

<SPONSOR>593

<CATEGORY>IM2-06

<TITLE>Anti-idiotypic-cytokine fusion protein for breast cancer therapy.

<LAST>Tripathi

<INIT>P.K.

<LAST>Qin

<INIT>H-X.

<LAST>Xu

<INIT>C.

<LAST>Foon

<INIT>K.A.

<LAST>Bhattacharya-Chatterjee

<INIT>M.

<LAST>Chatterjee

<INIT>S.K.

<AFFIL>Markey Cancer Center, University of Kentucky, Lexington, KY 40536

<ABSTRACT>We have generated a murine monoclonal anti-idiotypic antibody, 11D10, which mimicks biologically and antigenically a distinct and specific epitope of the high molecular weight human milk fat globule (HMFG). To augment the immunogenicity of 11D10 in vaccinated breast cancer patients, without using any carrier protein or adjuvant, we made a chimeric 11D10-GM-CSF fusion protein vaccine. An expression plasmid was made by ligation of the sequences of 11D10 light chain variable region, upstream of human κ constant region. The heavy chain plasmid was made by ligation of the heavy chain variable region sequences upstream of human γ 1 constant region CH1 and DNA fragment encoding the mature GM-CSF peptide to the 3' to the CH3 exon. P3 plasmocytoma cells were transfected with the light and heavy chain vectors by electroporation. Fusion protein was purified from culture media by chromatography in protein A columns and was separated on 7.5% non-reducing and 12.5% reducing SDS-polyacrylamide gels for western blotting. In non-reducing gel, a single band ~180 kd reacted with anti-human κ , anti-human λ 1 and anti-GM-CSF antibodies. In the reducing gel, a ~74 kd protein reacted with anti-human λ 1 and anti-GM-CSF antibodies. The fusion protein induced proliferation of GM-CSF dependent NFS-60 cells and strongly bound to anti-HMFG monoclonal antibody (Ab1). These results suggest that the protein is a chimeric anti-idiotypic antibody consisting of 11D10 variable domains, human κ and λ 1 constant domains. GM-CSF molecule is fused to γ 1 and is biologically active. Supported in part by NIH grant 1U01 CA 65748.

S. Chatterjee

```
===== 2179
Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>
Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTMP id 3791; Fri,
19 Jan 1996 17:33:18 -0500
Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP;
Fri, 19 Jan 96 17:33:13 EST
Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov
id RAA01409; Fri, 19 Jan 1996 17:33:11 -0500
Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6)
id RAA09963; Fri, 19 Jan 1996 17:33:09 -0500
Date: Fri, 19 Jan 1996 17:33:09 -0500
Message-Id: <199601192233.RAA09963@blaster.nlm.nih.gov>
To: SKCHAT00@UKCC.uky.edu
Subject: Results-BLAST Server
From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>
Errors-To: <owner-blast@ncbi.nlm.nih.gov>
Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>
```

```
--+=====
To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov'
with the word HELP in the body of the message. The documentation was last
modified March 18th.
```

```
--+=====
March 18, 1995
The BLAST FAQ was updated with the question Q33 related to degenerated
nucleotide code available for the BLAST programs.
```

```
--+=====
August 8, 1995
A new server directive ACKNOWLEDGE, has been added to the server. See the
help file for more details.
```

```
Trying blaster... connected
National Center for Biotechnology Information (NCBI)
```

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:31:12 EST 1996, Up 30 days, 5:22, 1 user, load: 42.14, 39.23, 35.07

PEPTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUpdate, updated daily
for efficient, complete searches of the five component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
swissprot SWISS-PROT Release 32.0, December 1995
pir PIR Release 45.0 (complete), June 30, 1995
spupdate SWISS-PROT cumulative weekly update to the major release
genpept CDS translations from GenBank(R) Release 92, December 15, 1995
gpupdate cumulative daily updates to the major release of genpept
kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995
tfd TFD transcription factor (protein) database Release 7.0, June 1993
alu * Translations of select Alu repeats from REPBASE
```

NUCLEOTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily
for efficient, complete searches of the four component databases:
pdb Brookhaven Protein Data Bank, April 1995 Release
genbank GenBank(R) Release 92 (no daily updates), December 15, 1995
gbupdate GenBank(R) cumulative daily updates to the major release
embl EMBL Data Library, Release 45.0, December 1995
emblu EMBL Data Library cumulative daily updates to the major release
vector Vector subset of GenBank(R), February 3rd, 1995
alu *+ Select Alu repeats from REPBASE
kabatnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
epd Eukaryotic Promoter Database Release 43, June 1995
dbest + Database of Expressed Sequence Tags (cumulative daily update)
dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994
```

- * Databases that are not accessible through the NCBI Retrieve E-mail server.
- + The TBLASTX program is restricted to searching these databases.

=====

You can obtain the BLAST documentation files, send a message consisting of just the word "help" (without the quotes) to: blast@ncbi.nlm.nih.gov
 Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

=====

For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

=====

A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov/>

=====

BLASTN 1.4.8MP [20-June-1995] [Build 08:41:09 Oct 19 1995]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= 11D10VH.nuc
 (354 letters)

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL
 662,343 sequences; 449,479,361 total letters.

Searching.....done

Observed Numbers of Database Sequences Satisfying
 Various EXPECTation Thresholds (E parameter values)

Histogram units: = 6 Sequences : less than 6 sequences

EXPECTation Threshold
 (E parameter)

EXPECTation Threshold (E parameter)	Observed Counts
10000	6848 336
6310	6512 204
3980	6308 167
2510	6141 156
1580	5985 99
1000	5886 135
631	5751 98
398	5653 106
251	5547 64
158	5483 77
100	5406 46
63.1	5360 162
39.8	5198 41
25.1	5157 101
15.8	5056 42
Expect = 10.0, Observed = 5014	
10.0	5014 137
6.31	4877 33
3.98	4844 59
2.51	4785 78
1.58	4707 70
1.00	4637 83
0.63	4554 110
0.40	4444 47

```

0.25 4397 99 |=====
0.16 4298 152 |=====
0.10 4146 65 |=====
0.063 4081 49 |=====
0.040 4032 24 |=====
0.025 4008 140 |=====
0.016 3868 93 |=====
0.010 3775 36 |=====
0.0063 3739 42 |=====
0.0040 3697 45 |=====
0.0025 3652 39 |=====
0.0016 3613 35 |=====

```

Sequences producing High-scoring Segment Pairs:				High Score	Smallest Sum Probability P(N)	N
gb L48668 MUSY	Mus musculus (cell line C3H/F2-20) c...	1337	2.9e-123	2		
gb L48680 MUSAL	Mus musculus (cell line C3H/F2-3) ch...	1301	1.3e-120	2		
emb x64805 MMAIDHCH	M.musculus mRNA for anti-Id mAB 114 ...	1473	2.6e-117	1		
gb M17953 MUSIGHXW	Mouse Ig rearranged H-chain V-region...	1350	1.7e-114	2		
gb I05921 I05921	Sequence 37 from patent EP 0274394. ...	1350	4.4e-114	2		
emb Z22117 MDIGGVBC	M.domesticus IgG variable region.	1127	7.4e-106	2		
gb M15224 MUSIGLAF	Mouse IgM H-chain lambda rearranged ...	1106	4.1e-104	2		
gb M15226 MUSIGLAH	H-chain lambda rearranged anti-Dns h...	1101	1.0e-103	2		
gb M15225 MUSIGLAG	H-chain lambda rearranged anti-Dns h...	1101	1.1e-103	2		
gb M20835 MUSIGKCLP	Mouse IgMk rearranged heavy-chain mR...	1093	3.8e-103	2		
emb Z22034 MDIGGVAG	M.domesticus IgG variable region.	1075	5.9e-103	2		
emb x59180 MMIGHT457	Mouse immunoglobulin variable region...	1098	7.3e-103	2		
emb Z25449 MMIGGCVR	M.musculus immunoglobulin gamma heav...	1299	9.1e-103	1		
emb Z25457 MMIGGCVR	M.musculus immunoglobulin gamma heav...	1298	1.1e-102	1		
gb L08216 MUSANTDNAK	Mouse anti-DNA antibody heavy chain ...	1098	4.7e-102	2		
emb A13735 A13735	variable region of a monoclonal anti...	1046	1.2e-101	2		
gb M20274 MUSIGHKA	Mouse Ig active gamma chain mRNA V-r...	1155	1.2e-101	2		
gb M32037 MUSIGHRK	Mouse Ig H-chain mRNA V-D-J region, ...	1155	1.2e-101	2		
gb M28834 MUSIGHALPA	Mus musculus IgG2a chain (anti-Pseud...	1046	1.2e-101	2		
gb M36225 MUSIGHAEF	Mouse Ig heavy-chain mRNA V region, ...	1284	1.4e-101	1		
gb U39781 MMU39781	Mus musculus J558+ IgM heavy chain m...	1073	2.3e-101	2		
emb Z25447 MMIGGCVRD	M.musculus immunoglobulin gamma heav...	1282	2.4e-101	1		
emb x65773 MMLB41HEV	M.musculus DNA for IgE antibody heav...	1279	2.8e-101	1		
gb U23046 MMU23046	Mus musculus, clone 2C10 anti-ds-DNA...	1071	3.2e-101	2		
emb Z12765 MM37F2A	M.musculus mRNA for VH-gen sequence ...	1086	3.9e-101	2		
gb U10410 MMU10410	Mus musculus recombinant antineurami...	1191	4.7e-101	2		
gb M32036 MUSIGHRJ	Mouse Ig H-chain mRNA V-D-J region, ...	1146	6.8e-101	2		
emb Z68170 MMVAR605	M.musculus mRNA for immunoglobulin h...	1065	1.0e-100	2		
gb L08220 MUSANTDNAO	Mouse anti-DNA antibody heavy chain ...	1071	1.5e-100	2		
gb M19292 MUSIGHXK	Mouse IgG active H-chain gene VDJ2-r...	1142	1.5e-100	2		
emb Z22028 MDIGGVAD	M.domesticus IgG variable region.	1071	1.8e-100	2		
gb L24557 MUSIGHMADQ	Mus musculus (S03) monoclonal anti-H...	1051	3.1e-100	2		
gb J00493 MUSIGHAP	Mouse Ig active H-chain V-region fro...	1137	3.2e-100	2		
gb M32035 MUSIGHRI	Mouse Ig H-chain mRNA V-D-J region, ...	1137	3.8e-100	2		
emb x75095 MMHCVR1	M.musculus (A.SW) mRNA for antibody ...	1137	3.8e-100	2		
emb Z22088 MDIGGVAR	M.domesticus IgG variable region.	1056	3.9e-100	2		
gb M97876 MUSL771GHV	Mouse hybridoma Ig rearranged H-chai...	1066	4.3e-100	2		
gb M61026 MUSIGHAANN	M.musculus Ig rearranged H-chain mRN...	1266	4.4e-100	1		
emb Z12794 MMV20552B	M.musculus mRNA for VH-gen sequence ...	1057	4.5e-100	2		
emb Z12799 MMV20652B	M.musculus mRNA for VH-gen sequence ...	1057	4.5e-100	2		
emb Z22129 MDIGMVBC	M.domesticus IgM variable region.	1057	4.6e-100	2		
emb Z22134 MDIGMVBF	M.domesticus IgM variable region.	1063	8.2e-100	2		
gb M64141 MUSIGHNOL	Mouse Ig active heavy-chain mRNA V-r...	1046	8.8e-100	2		
gb I09505 I09505	Sequence 3 from patent WO 8909622.	1107	9.8e-100	2		
gb M31908 MUSIGHRC	Mouse Ig H-chain V-D-J region mRNA, ...	1132	9.9e-100	2		
gb M28251 MUSIGHMX	Mouse Ig rearranged gamma-chain (G-2...	1107	1.1e-99	2		
emb Z12783 MMV20292B	M.musculus mRNA for VH-gen sequence ...	1052	1.2e-99	2		
gb M36215 MUSIGHADV	Mouse Ig heavy-chain mRNA V region, ...	1060	1.2e-99	2		
emb A23297 A23297	M.musculus CTM01 monoclonal antibody...	1073	1.5e-99	2		

emb	Z12798	MMV20642B	M.musculus mRNA for VH-gen sequence ...	1048	2.5e-99	2
emb	Z29586	MMIGMUHCV	M.musculus (NZB X NZW)F1 mRNA for Im...	1052	5.6e-99	2
emb	X68118	MMIGHPS4A	M.musculus gene for IG heavy chain (...)	1122	6.6e-99	2
gb	M31286	MUSIGHAUA	Mouse active rheumatoid factor IgG2B...	1093	7.0e-99	2
emb	X62706	MMIG2832G	M.musculus mRNA for anti-estrogen re...	1032	8.0e-99	2
emb	X75100	MMASWU1H	M.musculus (A.SW) mRNA for ASWU1 ant...	1130	1.0e-98	2
emb	Z22059	MDIGGVAN	M.domesticus IgG variable region.	1114	1.2e-98	2
gb	M12809	MUSIGHJA	Mouse Ig rearranged H-chain V-region...	1119	1.2e-98	2
emb	X56936	MMSP6718	Mouse rearranged Sp6-718 gene for Ig...	1110	1.4e-98	2
emb	Z12792	MMV20512B	M.musculus mRNA for VH-gen sequence ...	1048	1.4e-98	2
gb	M64134	MUSIGHNOE	Mouse Ig active heavy-chain mRNA V-r...	1084	1.5e-98	2
gb	J04548	MUSIGHVBE	Mouse Ig active gamma-1-chain mRNA, ...	1114	1.7e-98	2
emb	Z25445	MMIGGCVRG	M.musculus immunoglobulin gamma heav...	1247	2.1e-98	1
gb	J04547	MUSIGHVBD	Mouse Ig active gamma-2a mRNA, VNDJ2...	1114	2.5e-98	2
emb	Z25443	MMIGGCVRB	M.musculus immunoglobulin gamma heav...	1246	2.5e-98	1
emb	Z22099	MDIGGVAV	M.domesticus IgG variable region.	1115	2.5e-98	2
emb	Z25453	MMIGGCVRG	M.musculus immunoglobulin gamma heav...	1246	2.5e-98	1
emb	X68122	MMIGHPS6A	M.musculus gene for IG heavy chain (...)	1114	3.0e-98	2
gb	M83098	MUSIGHM195	Mus musculus Ig heavy chain mRNA V-r...	1039	3.3e-98	2
gb	M64142	MUSIGHNOM	Mouse Ig active heavy-chain mRNA V-r...	1083	4.9e-98	2
gb	L08985	MUSIGVAAM	Mus musculus Ig rearranged anti-Sm h...	622	6.2e-98	4
emb	X68112	MMIGHPS1A	M.musculus gene for IG heavy chain (...)	1110	6.6e-98	2
emb	Z12763	MM2F2A	M.musculus mRNA for VH-gen sequence ...	1239	7.7e-98	1
emb	Z25451	MMIGGCVRG	M.musculus immunoglobulin gamma heav...	1240	7.7e-98	1
gb	M31956	MUSIGHRO	Mouse Ig active mu-chain mRNA V-D-J2...	1109	7.9e-98	2
emb	Z12774	MMV162B	M.musculus mRNA for VH-gen sequence ...	1038	9.7e-98	2
emb	Z12789	MMV20442B	M.musculus mRNA for VH-gen sequence ...	1029	9.7e-98	2
gb	L35315	MUS1VDJA	Mus musculus germline immunoglobulin...	1107	9.9e-98	2
gb	U26469	MMU26469	Mus musculus nucleosome-reactive mon...	1037	1.2e-97	2
gb	S72514	S72514	anti-estradiol antibody heavy chain ...	1024	1.3e-97	2
gb	L25855	MUSIGGB	Mus musculus IgG heavy chain gene, V...	1101	1.7e-97	2
gb	S69279	S69279	IgVH=anti-louping ill virus antibody...	1081	2.1e-97	2
gb	U40581	MMU40581	Mus musculus sFv antibody mRNA, cont...	1098	2.6e-97	2
gb	M34581	MUSIGHABU	Mouse Ig heavy-chain mRNA V-D-J regi...	1102	3.0e-97	2
emb	X82581	MMIGPE2	M.musculus mRNA for immunoglobulin h...	1067	3.2e-97	2
emb	X63799	MMVHMRB6	M.musculus mRNA for IgM V(H)MRB6	1030	3.6e-97	2
emb	X68116	MMIGHPS3A	M.musculus gene for IG heavy chain (...)	1101	3.7e-97	2
gb	L22749	MUS1	Mus musculus immunoglobulin heavy ch...	1230	4.3e-97	1
gb	U41425	MMU41425	Mus musculus monoclonal antibody FC1...	1114	5.7e-97	2
emb	Z21788	MMIGGAA	M.musculus Biozzi immunoglobulin gam...	1019	6.2e-97	2
gb	S74051	S74051	Ig VH=anti-cardiolipin immunoglobuli...	1228	6.5e-97	1
gb	U22903	MMU22903	Mus musculus anti-human interferon-g...	1076	7.4e-97	2
emb	X68120	MMIGHPS5A	M.musculus gene for IG heavy chain (...)	1096	9.4e-97	2
gb	L48669	MUSZ	Mus musculus (cell line C3H/F2-21) c...	1025	1.2e-96	2
gb	J04546	MUSIGHVBC	Mouse Ig active gamma-2a-chain mRNA,...	1094	1.4e-96	2
gb	U26470	MMU26470	Mus musculus nucleosome-reactive mon...	1017	1.4e-96	2
emb	X68114	MMIGHPS2A	M.musculus gene for IG heavy chain (...)	1092	2.0e-96	2
emb	X65004	MMIHLG43	M.musculus rearranged immunoglobulin...	1037	2.4e-96	2
emb	Z12771	MM7A1	M.musculus mRNA for VH-gen sequence ...	1221	2.4e-96	1
gb	U20819	MMU20819	Mus musculus Ig Fab F9.13.7 heavy ch...	1001	2.6e-96	2
emb	X03088	MMIGMU32	Mouse rearranged V(H) gene VMU-3.2 V...	1091	2.6e-96	2

WARNING: Descriptions of 4914 database sequences were not reported due to the limiting value of parameter V = 100.

>gb|L48668|MUSY Mus musculus (cell line C3H/F2-20) chromosome 12 anti-DNA antibody heavy chain mRNA.
Length = 357

Plus Strand HSPs:

Score = 1337 (369.4 bits), Expect = 2.9e-123, Sum P(2) = 2.9e-123
Identities = 279/294 (94%), Positives = 279/294 (94%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

```

Sbjct: 1 CAGGCTTATNTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
Query: 121 CCTGGACAGGGCCTGGAATGGATTGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
Sbjct: 121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTAC 180
Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
Sbjct: 181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240
Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294

```

Score = 221 (61.1 bits), Expect = 2.9e-123, Sum P(2) = 2.9e-123
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 312 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

```

>gb|L48680|MUSAL Mus musculus (cell line C3H/F2-3) chromosome 12 anti-DNA
antibody heavy chain mRNA.
Length = 360

Plus Strand HSPs:

Score = 1301 (359.5 bits), Expect = 1.3e-120, Sum P(2) = 1.3e-120
Identities = 277/298 (92%), Positives = 277/298 (92%), Strand = Plus / Plus

```

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCCTCAGTGAAGATG 60
Sbjct: 1 CAGGCTTATGTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 60
Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACAGATTTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
Query: 121 CCTGGACAGGGCCTGGAATGGATTGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
Sbjct: 121 CGTAGACAGGGCCTGGAATGGATTGGAGCAATTTATCCAGGAAATGGTGATACTTCCTAT 180
Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
Sbjct: 181 AATCAGAAGTTCAAGGGCAAGGCCACACTGATTGTAGACAAATCCTCCAGCACAGCCTAC 240
Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 298
Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGAGA 298

```

Score = 225 (62.2 bits), Expect = 1.3e-120, Sum P(2) = 1.3e-120
Identities = 53/63 (84%), Positives = 53/63 (84%), Strand = Plus / Plus

```

Query: 292 AGAGGGAAGTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351
Sbjct: 298 AGGGGTAACTACGTAGGACATATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 357
Query: 352 TCA 354
Sbjct: 358 TCA 360

```

>emb|X64805|MMAIDHCH M.musculus mRNA for anti-Id mAB 114 heavy chain, variable region
Length = 354

Plus Strand HSPs:

Score = 1473 (407.0 bits), Expect = 2.6e-117, P = 2.6e-117
Identities = 321/354 (90%), Positives = 321/354 (90%), Strand = Plus / Plus

```

Query:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
          |||||
Sbjct:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTAAGGCTGGGTCTCAGTGAAGATG 60

Query:   61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
          |||||
Sbjct:   61 TCCTGCAAGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
          |||||
Sbjct:   121 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTAC 180

Query:   181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
          |||||
Sbjct:   181 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAAC 300
          |||||
Sbjct:   241 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAT 300

Query:   301 TGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
          |||||
Sbjct:   301 TACTCCGTTAGTATAGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 354

```

>gb|M17953|MUSIGHXW Mouse Ig rearranged H-chain V-region mRNA VJ1.
Length = 458

Plus Strand HSPs:

Score = 1350 (373.0 bits), Expect = 1.7e-114, Sum P(2) = 1.7e-114
Identities = 282/297 (94%), Positives = 282/297 (94%), Strand = Plus / Plus

```

Query:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
          |||||
Sbjct:   96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCCTCAGTGAAGATG 155

Query:   61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
          |||||
Sbjct:   156 TCCTGCAAGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215

Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
          |||||
Sbjct:   216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTAC 275

Query:   181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
          |||||
Sbjct:   276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
          |||||
Sbjct:   336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392

```

Score = 101 (27.9 bits), Expect = 1.7e-114, Sum P(2) = 1.7e-114
Identities = 25/31 (80%), Positives = 25/31 (80%), Strand = Plus / Plus

```

Query:   321 CTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351
          |||||
Sbjct:   428 CTGGGGCACAGGGACCACGGTCACCGTCTCC 458

```

>gb|I05921|I05921 Sequence 37 from patent EP 0274394. >gb|I08811|I08811
Sequence 12 from patent WO 8804936. >gb|I09199|I09199 Sequence 38
from patent WO 8900999.
Length = 458

Plus Strand HSPs:

Score = 1350 (373.0 bits), Expect = 4.4e-114, Sum P(2) = 4.4e-114
Identities = 282/297 (94%), Positives = 282/297 (94%), Strand = Plus / Plus

```
Query:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
          |||||
Sbjct:  96 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCCTGGGGCCTCAGTGAAGATG 155

Query:   61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
          |||||
Sbjct:  156 TCCTGCAAGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACA 215

Query:   121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
          |||||
Sbjct:  216 CCTAGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTTAC 275

Query:   181 AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
          |||||
Sbjct:  276 AATCAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTAC 335

Query:   241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
          |||||
Sbjct:  336 ATGCAGCTCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGTG 392
```

Score = 96 (26.5 bits), Expect = 4.4e-114, Sum P(2) = 4.4e-114
Identities = 24/30 (80%), Positives = 24/30 (80%), Strand = Plus / Plus

```
Query:   321 CTGGGGTCAAGGAACCTCAGTCACCGTCTC 350
          |||||
Sbjct:  428 CTGGGGCACAGGGACCACGGTCACCGTCTC 457
```

>emb|Z22117|MDIGGVBC M.domesticus IgG variable region.
Length = 360

Plus Strand HSPs:

Score = 1127 (311.4 bits), Expect = 7.4e-106, Sum P(2) = 7.4e-106
Identities = 258/300 (86%), Positives = 259/300 (86%), Strand = Plus / Plus

```
Query:   2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
          |||||
Sbjct:  2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATAT 61

Query:   62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
          |||||
Sbjct:  62 CCTGCAAGGCTTCTGGATACACATTCACTGACTACTACATGCACTGGGTAAAGCAGAAGC 121

Query:   122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
          |||||
Sbjct:  122 CTGGGCAGGGCCTTGAGTGGATTGGAGAGATTATCCTGGAAGTGGTAATACTTACTACA 181

Query:   182 ATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
          |||||
Sbjct:  182 ATGAGAAGTTCAAGGGYAAGGCCCTACTGACTGCAGACAAATCCTCCAGCACAGCCTACA 241

Query:   242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
          |||||
Sbjct:  242 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGACGTTACT 301
```

Score = 221 (61.1 bits), Expect = 7.4e-106, Sum P(2) = 7.4e-106
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15224|MUSIGLAF Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ4
region of J558 family mRNA.
Length = 360

Plus Strand HSPs:

Score = 1106 (305.6 bits), Expect = 4.1e-104, Sum P(2) = 4.1e-104
Identities = 254/295 (86%), Positives = 254/295 (86%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
|||||
Sbjct: 1 CAGGTTCAAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
|||||
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
|||||
Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTATCCTGGAGATGGTGATACTAGGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
|||||
Sbjct: 181 ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAG 295
|||||
Sbjct: 241 ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAG 295

Score = 221 (61.1 bits), Expect = 4.1e-104, Sum P(2) = 4.1e-104
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
|||||
Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M15226|MUSIGLAH H-chain lambda rearranged anti-Dns hybridoma VDJ4 region of
J558 family mRNA.
Length = 363

Plus Strand HSPs:

Score = 1101 (304.2 bits), Expect = 1.0e-103, Sum P(2) = 1.0e-103
Identities = 253/294 (86%), Positives = 253/294 (86%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
|||||
Sbjct: 1 CAGGTTCAAGCTCCAGCAGTCTGGGGCTGAGCTGGCAAGACCTGGGGCTTCAGTGAAGTTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
|||||
Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
|||||
Sbjct: 121 CCTGGACAGGGTCTGGAATGGATTGGGGCTATTATCCTGGAGATGGTGATACTAGGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
|||||

Sbjct: 166 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGCTACTGGATAAACTGGGTGAAGCAGAGG 225

Query: 13 CAGCAGTCTGGGGCTGAGCTGGTGAGGCTGGGGCTCAGTGAAGATGTCTGCAAGGCT 72
 |||
 Sbjct: 3 CAGCAGTCTGGGCTGAGCTGGTGAGGCTGGAGCTCAGTGAAGCTGTCTGCAAGGCT 62

Query: 73 TCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGC 132
 |||||
 Sbjct: 63 TCTGGCTACACATTCAACAGCTACTGGATGCACTGGGTGAAGCAGAGGCATGGACAAGGC 122

Query: 133 CTGGAATGGATTGGAATATTTTCTGGAATGGTGATACTTACTACAATCAGAAGTTT 192
 |||||
 Sbjct: 123 CTTGAGTGGATTGGAATATTTATCCTGGTAGTGGTAGTACTAAGTACGATGAGAAGTTC 182

Query: 193 AAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGC 252
 |||||
 Sbjct: 183 AAGAGCAAGGGCACACTGACTGTAGACACATCCTCCAGCACAGCCTACATGCACCTCAGC 242

Query: 253 AGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGTGGGAGGGT 309
 |||||
 Sbjct: 243 AGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTACAAGAGAGGAGGATGATGGT 299

Score = 214 (59.1 bits), Expect = 7.3e-103, Sum P(2) = 7.3e-103
 Identities = 46/50 (92%), Positives = 46/50 (92%), Strand = Plus / Plus

Query: 305 AGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 301 ACGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCAGTCTCTCCTCA 350

>emb|225449|MMIGGCVRE M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
 v region.
 Length = 305

Plus Strand HSPs:

Score = 1299 (358.9 bits), Expect = 9.1e-103, P = 9.1e-103
 Identities = 275/294 (93%), Positives = 275/294 (93%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
 |||||
 Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCA 67

Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
 |||||
 Sbjct: 68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127

Query: 128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAATGGTGATACTTACTACAATCAGA 187
 |||||
 Sbjct: 128 AGGGCCTGGAATGGATTGAGCTATTTATCCAGGAAATGGTGATACTTCTACAATCAGA 187

Query: 188 AGTTTAAGGGCAAGGCCTATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
 |||||
 Sbjct: 188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247

Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
 |||||
 Sbjct: 248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGTTACT 301

>emb|225457|MMIGGCVRI M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
 v region.
 Length = 302

Plus Strand HSPs:

Score = 1298 (358.7 bits), Expect = 1.1e-102, P = 1.1e-102
 Identities = 274/292 (93%), Positives = 274/292 (93%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
 |||||
 Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCA 67

```

Query:      68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
             |||
Sbjct:      68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
             |||

Query:     128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187
             |||
Sbjct:     128 AGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCTACAATCAGA 187
             |||

Query:     188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
             |||
Sbjct:     188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247
             |||

Query:     248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAA 299
             |||
Sbjct:     248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGGA 299
             |||

```

>gb|L08216|MUSANTDNAK Mouse anti-DNA antibody heavy chain variable region (J558
VH family) mRNA.
Length = 366

Plus Strand HSPs:

Score = 1098 (303.4 bits), Expect = 4.7e-102, Sum P(2) = 4.7e-102
Identities = 254/297 (85%), Positives = 254/297 (85%), Strand = Plus / Plus

```

Query:      1  CAGGCTATCTACAGCAGCTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||
Sbjct:      1  CAGGTTCAGCTCCAGCAGCTCTGGGGCTGAGCTGGCCAGACCTGGGGCTTCAGTGAAGTTG  60

Query:     61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCAGCTGGGTAAAGCAGACA  120
             |||||
Sbjct:     61  TCCTGCCAGGCTTCTGGCTACACCTTTACCAGCTACTGGATGCAGTGGGTAAACAGAGG  120

Query:    121  CCTGGACAGGGCCTGGAATGGATTGAAATATTTTTCTGAAATGGTGATACTTACTAC  180
             |||||
Sbjct:    121  CCTGGACAGGGCCTGGAATGGATTGGGCCTATTTATCCTGGAGATGGTGATACTAGGTAC  180

Query:    181  AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCTCCAGCACAGCCTAC  240
             |||||
Sbjct:    181  ACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCTCCAGCACAGCCTAC  240

Query:    241  ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG  297
             |||||
Sbjct:    241  ATGCAACTCAGCAGCTTGGCATCTGAGGACTCTGCGGTCTATTACTGTACAAATGGG  297

```

Score = 204 (56.4 bits), Expect = 4.7e-102, Sum P(2) = 4.7e-102
Identities = 44/48 (91%), Positives = 44/48 (91%), Strand = Plus / Plus

Query: 307 GGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 319 GATGCTATGGGCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCA 366

>emb|A13735|A13735 variable region of a monoclonal antibody which cross reacts
with 19 known *Pseudomonas aeruginosa* serotypes.
Length = 540

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 250/301 (83%), Positives = 250/301 (83%), Strand = Plus / Plus

```

Query:      1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||  ||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     121 CAGGTCACAGCTTCAGCAGTCTGGGGCTGAAC TGGCAAACCTGGGGCCTCAGTGAAGATG  180

Query:     61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAGCAGACA  120

```

```

Sbjct: 181 TCCTGCAAGGCTCTCGCTACACCTTTACTGCCTACTGGATGCACCTGGGTAACACAGAGG 240
Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
Sbjct: 241 CCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAACACTGGTTATACTGAATAC 300
Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
Sbjct: 301 AATCAGAACTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 360
Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAC 300
Sbjct: 361 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTATTGTACAAGAAGCTAC 420
Query: 301 T 301
Sbjct: 421 T 421

```

Score = 249 (68.8 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 53/57 (92%), Positives = 53/57 (92%), Strand = Plus / Plus

Query: 298 AACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 424 AACTACGAGGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 480

>gb|M20274|MUSIGHKA Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 36-65. >gb|M20275|MUSIGHKB Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 4F8. >gb|M20276|MUSIGHKC Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 26C2. >gb|M20277|MUSIGHKD Mouse Ig active gamma chain mRNA V-region VD_JH2, partial cds, clone 24F3. >emb|X06110|MMJGVHD1 Mouse mRNA (36-35) for immunoglobulin heavy chain VD_J-region
Length = 363

Plus Strand HSPs:

Score = 1155 (319.1 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 271/321 (84%), Positives = 271/321 (84%), Strand = Plus / Plus

```
Query:      2 AGGCTTATCTACAGCAGCTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCCTCAGTGAAGATGT 61
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      2 AGGTTCAAGCTTCAGCAGCTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query:     62 CCTGCAAGGCCTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     62 CCTGCAAGGCCTCTGGATATACATTCAACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:    122 CTGGACAGGGCCTGGAATGGATTGGAATATTTTTCTGGAAATGGTGATACTTACTACA 181
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    122 CTGGACAGGGCCTGGAATGGATTGGATATATTAACTCGGAAATGGTTATACTAAGTACA 181

Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCAT TGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:    242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCGGTCT 301

Query:    302 GGGAGGGTGCTCTGGACTACT 322
             || | | | | | | | | |
Sbjct:    302 ACTATGGTGGTAGTTACTACT 322
```

Score = 142 (39.2 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

>gb|M32037|MUSIGHRK Mouse Ig H-chain mRNA V-D-J region, from hybridoma P6514-2,
 partial cds. >gb|M32038|MUSIGHRL Mouse Ig H-chain mRNA V-D-J
 region, from hybridoma P65J4-1, partial cds.
 Length = 363

Plus Strand HSPs:

Score = 1155 (319.1 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 271/321 (84%), Positives = 271/321 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
 |||||
 Sbjct: 2 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
 |||||
 Sbjct: 62 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query: 122 CTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACA 181
 |||||
 Sbjct: 122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATACTAAGTACA 181

Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
 |||||
 Sbjct: 182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
 |||||
 Sbjct: 242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCTAATT 301

Query: 302 GGGAGGGTGCTCTGGACTACT 322
 |||||
 Sbjct: 302 ACTATGGTGGTAGCTACTACT 322

Score = 142 (39.2 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

>gb|M28834|MUSIGHALPA Mus musculus IgG2a chain (anti-Pseudomonas aeruginosa
 lipoprotein I antibody) mRNA, 5' end.
 Length = 525

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
 Identities = 250/301 (83%), Positives = 250/301 (83%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 106 CAGGTCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAAGATG 165

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 166 TCCTGCAAGGCTTCTGGCTACACCTTTACTGCCTACTGGATGCACTGGGTAAACAGAGG 225

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 226 CCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAACACTGGTTATACTGAATAC 285

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 286 AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 345

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 346 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTATTGTACAAGAAGCTAC 405

Query: 301 T 301

Sbjct: 406 T 406

Score = 249 (68.8 bits), Expect = 1.2e-101, Sum P(2) = 1.2e-101
Identities = 53/57 (92%), Positives = 53/57 (92%), Strand = Plus / Plus

Query: 298 AACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 409 AACTACGAGGGGGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 465

>gb|M36225|MUSIGHAEF Mouse Ig heavy-chain mRNA V region, partial cds.
H280-15VH.
Length = 354

Plus Strand HSPs:

Score = 1284 (354.8 bits), Expect = 1.4e-101, P = 1.4e-101
Identities = 300/354 (84%), Positives = 300/354 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAAACCTGGGGCCTCAGTGAAGATG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCACTGGGTAAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCTGGAATGGATTGGATACATTAATCCTAGCACTGGTTATACTGAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCACTGTATTACTGTGCAAGATGGGTC 300

Query: 301 TGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 301 TATTACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

>gb|U39781|MMU39781 Mus musculus J558+ IgM heavy chain mRNA, hybridoma clone
ME2B7, partial cds.
Length = 339

Plus Strand HSPs:

Score = 1073 (296.5 bits), Expect = 2.3e-101, Sum P(2) = 2.3e-101
Identities = 245/283 (86%), Positives = 245/283 (86%), Strand = Plus / Plus

Query: 19 TCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGC 78

Sbjct: 1 TCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAAGTGAAGATGTCCTGCAAGGCTTCTGGC 60

Query: 79 TACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAA 138

```

Sbjct: 61 TACACCTTACCAGCTACTGGATAACCTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAG 120
Query: 139 TGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACAATCAGAAGTTAAGGGC 198
Sbjct: 121 TGGATTGGAGATATTATCCTGGTAGTGGTAGTACTAACTACAATGAGAAGTTCAAGAGC 180
Query: 199 AAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGCAGCCTG 258
Sbjct: 181 AAGGCCACACTGACTGTAGACACATCCTCCAGCACAGTCTACATGCAGCTCAGCAGCCTG 240
Query: 259 ACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
Sbjct: 241 ACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATGGATCT 283

```

Score = 221 (61.1 bits), Expect = 2.3e-101, Sum P(2) = 2.3e-101
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 294 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 339

```

>emb|225447|MMIGCVRD M.musculus immunoglobulin gamma heavy chain (DBA/1) gene,
v region.
Length = 303

Plus Strand HSPs:

Score = 1282 (354.2 bits), Expect = 2.4e-101, P = 2.4e-101
Identities = 270/287 (94%), Positives = 270/287 (94%), Strand = Plus / Plus

```

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
Sbjct: 8 AACTGCAGCAGCCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67
Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
Sbjct: 68 AGGCTTCTGGCTACACATTACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127
Query: 128 AGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187
Sbjct: 128 AGGGCCTGGAATGGATTGGAGCTATTATCCAGGAAATGGTGATACTTCTACAATCAGA 187
Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247
Sbjct: 188 AGTTCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGC 247
Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
Sbjct: 248 TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 294

```

>emb|X65773|MMLB41HEV M.musculus DNA for IgE antibody heavy chain (VDJ)
Length = 451

Plus Strand HSPs:

Score = 1279 (353.4 bits), Expect = 2.8e-101, P = 2.8e-101
Identities = 299/353 (84%), Positives = 299/353 (84%), Strand = Plus / Plus

```

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct: 99 AGGTCCAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGCCTGGGTCTCAGTGAAGATGT 158
Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct: 159 CCTGCAAGAGTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAGCAGAGGC 218

```

Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCCTGGAAATGGTGATACTTACTACA 181
 |||||
 Sbjct: 219 CTGGACAGGGCCTGGAATGGATTGGATATATTTATATTGGATATGGTTATATTGAGTATA 278
 |||||
 Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
 |||||
 Sbjct: 279 ATGAGAAGTTCAAGGGCAAGGCCACACTGACTTCAGACACATCCTCCAGGACAGCCTACA 338
 |||||
 Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
 |||||
 Sbjct: 339 TGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCAATCTATTTCTGTGCAAGATGGGGCT 398
 |||||
 Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 399 TAATCTTTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 451
 |||||

>gb|U23046|MMU23046 Mus musculus, clone 2C10 anti-ds-DNA immunoglobulin heavy
 chain V region, partial cds.
 Length = 360

Plus Strand HSPs:

Score = 1071 (295.9 bits), Expect = 3.2e-101, Sum P(2) = 3.2e-101
 Identities = 251/297 (84%), Positives = 251/297 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 1 CAGGTCCAACCTACAGCAGCCTGGTGCTGAGCTTGGAAGCCTGGGGCCTCAGTGAAGCTG 60
 |||||
 Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACTTTCACCAGGTTCTGGATAAAGTGGTGAGGCAGAGG 120
 |||||
 Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTGGACAAGGCCTTGAGTGGATTGGAAATATTTATCCTGGTAGTAGTAGTATTAACCTAC 180
 |||||
 Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATGAGAAGTTCAAGAACAAGGCCACACTGACTGTAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGACGACTCTGCGGTCTATTATTGTGCAAGACGG 297
 |||||

Score = 221 (61.1 bits), Expect = 3.2e-101, Sum P(2) = 3.2e-101
 Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 315 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360
 |||||

>emb|Z12765|MM37F2A M.musculus mRNA for VH-gen sequence of naturally occurring,
 somatically mutated memory B cell
 Length = 363

Plus Strand HSPs:

Score = 1086 (300.1 bits), Expect = 3.9e-101, Sum P(2) = 3.9e-101
 Identities = 258/309 (83%), Positives = 258/309 (83%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAGGCCTGGGTCTCAGTGAAGCTG 60
 |||||

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCATTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTATACAAGGCCTTGAATGGATTGGTAACATTGACCCTTCTGATAGTGAACTCACTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATCAAAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAATCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGAGAGC 300

Query: 301 TGGGAGGGT 309
 |||||
 Sbjct: 301 TACTATGGT 309

Score = 205 (56.6 bits), Expect = 3.9e-101, Sum P(2) = 3.9e-101
 Identities = 45/50 (90%), Positives = 45/50 (90%), Strand = Plus / Plus

Query: 305 AGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 314 ACGGGCTATGGACTACTGGGGCCAGGGAACCTCAGTCACCGTCTCCTCA 363

>gb|U10410|MMU10410 Mus musculus recombinant antineuraminidase single chain Ig
 VH and VL domains mRNA, complete cds.
 Length = 831

Plus Strand HSPs:

Score = 1191 (329.1 bits), Expect = 4.7e-101, Sum P(2) = 4.7e-101
 Identities = 263/294 (89%), Positives = 263/294 (89%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
 |||||
 Sbjct: 67 CAGGTGCAGCTGCAGCAGTCTGGGGCTGAACTGGTGAAGCCTGGGGCCTCAGTGAGGATG 126

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 127 TCCTGCAAGGCTTCTGGCTACACATTTACCAATTACAACATGTACTGGGTAAACAGTCA 186

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 187 CCTGGACAGGGCCTGGAGTGGATTGGAATTTTATCCAGGAAATGGTGATACTTCTTAC 246

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 247 AATCAGAAGTTCAAAGACAAGGCCACATTGACTGCTGACAAATCCTCCAACACAGCCTAC 306

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
 |||||
 Sbjct: 307 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGA 360

Score = 150 (41.4 bits), Expect = 4.7e-101, Sum P(2) = 4.7e-101
 Identities = 38/48 (79%), Positives = 38/48 (79%), Strand = Plus / Plus

Query: 304 GAGGGTCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCC 351
 |||||
 Sbjct: 382 GACGGAGGCTTTGACTACTGGGGCAAGGGACCACGGTCACCGTCTCC 429

>gb|M32036|MUSIGHRJ Mouse Ig H-chain mRNA V-D-J region, from hybridoma P65D6-3,
 partial cds.
 Length = 363

Plus Strand HSPs:

Score = 1146 (316.7 bits), Expect = 6.8e-101, Sum P(2) = 6.8e-101
Identities = 270/321 (84%), Positives = 270/321 (84%), Strand = Plus / Plus

```

Query:   2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   2 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGCTCCTCAGTGAAGATGT 61

Query:  62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  62 CCTGCAAGGCTTCTGGATATACATTCAAGCTACGGTATAAAGTGGGTGAAACAGAGGC 121

Query:  122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATACTAAGTACA 181

Query:  182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:  242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCCCATT 301

Query:  302 GGGAGGGTGCTCTGGACTACT 322
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  302 ACTATGGTGGTAGCTACTACT 322

```

Score = 142 (39.2 bits), Expect = 6.8e-101, Sum P(2) = 6.8e-101
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

```

Query:  314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

```

>emb|Z68170|MMVAR605 M.musculus mRNA for immunoglobulin heavy chain variable region (clone 605). >emb|Z68170|MMVAR605 M.musculus mRNA for immunoglobulin heavy chain variable region (clone 605)
Length = 363

Plus Strand HSPs:

Score = 1065 (294.3 bits), Expect = 1.0e-100, Sum P(2) = 1.0e-100
Identities = 249/294 (84%), Positives = 249/294 (84%), Strand = Plus / Plus

```

Query:   1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   1 CAGGTCAAGCTGCAGCAGTCAAGGACTGTGCTGGCAAGGCCTGGGGCTTCAAGTGAAGATG 60

Query:  61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTAAACAGAGG 120

Query:  121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  121 CCTGGACAGGGCTGGAATGGATTGGCGCTATTTATCCTGGAAATAGTGATACTAGCTAC 180

Query:  181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  181 AACCAAGAAGTTCAAGGGCAAGGCCAACTGACTGCAGTACATCCACCAGCACTGCCTAC 240

Query:  241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:  241 ATGGAGCTCAGCAGCCTGACAAATGAGGACTCTGCGGTCTATTACTGTACAAGA 294

```

```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATGT 61
             |||
Sbjct:      2 AGGTTCAAGCTTCTGAGCTCTGGAGCTGAGCTGGTGAGGGCTGGGTCCTCAGTGAAGATGT 61

Query:     62 CTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             |||
Sbjct:     62 CTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:    122 CTGGACAGGGCCTGGAATGGATTGGAATATTTTTCTCGAAATGGTGATACTTACTACA 181
             |||
Sbjct:    122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCTCGAAATGGTTATACTAAGTACA 181

Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             |||

```

Sbjct: 182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 301

Sbjct: 242 TGCAGCTCAGAAGCCTGACATCTGAGGAYTCTGCAGTCTATTTCTGCGCAAGATCGGTCT 301

Query: 302 GGGAGGGTGCTCTGGACTACT 322

Sbjct: 302 ACTATGGTGGTAGTTACTACT 322

Score = 142 (39.2 bits), Expect = 1.5e-100, Sum P(2) = 1.5e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 323 TTGACTACTGGGGCCAAGGCACCACTCTCAGTCTCCTCA 363

>emb|222028|MDIGGVAD M.domesticus IgG variable region.
Length = 363

Plus Strand HSPs:

Score = 1071 (295.9 bits), Expect = 1.8e-100, Sum P(2) = 1.8e-100
Identities = 251/297 (84%), Positives = 251/297 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61

Sbjct: 2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGTTGGTAAAGCCTGGGGCCTCAGTGAAGATGT 61

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121

Sbjct: 62 CCTGCAAGGCTTCTGGATACACATTCAGTAGATATGTTATGCACTGGGTAAAGCAGAAAGC 121

Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAATGGTGATACTTACTACA 181

Sbjct: 122 CTGGGACAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAATACA 181

Query: 182 ATCAGAAGTTTAAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241

Sbjct: 182 ATGAGAAGTTCAAAGGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241

Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGA 298

Sbjct: 242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAGGGA 298

Score = 212 (58.6 bits), Expect = 1.8e-100, Sum P(2) = 1.8e-100
Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 318 TGCTATGGACTACTGGGGTCAAGGAGCCTCAGTCACCGTCTCCTCA 363

>gb|L24557|MUSIGHMADQ Mus musculus (S03) monoclonal anti-HLA-DQ3 monoclonal
antibody IgH chain mRNA, V-region.
Length = 368

Plus Strand HSPs:

Score = 1051 (290.4 bits), Expect = 3.1e-100, Sum P(2) = 3.1e-100
Identities = 247/293 (84%), Positives = 247/293 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61

Sbjct: 1 AGGTCAAGCTCAGGAGTCAGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGT 60

Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121

```

Sbjct: 61 CCTGCAAGGCTTCTGGCTACACCTTTAGTAGGTAAGTGCATGGGTGAAACAGCGGC 120
Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct: 121 CTGGACAGGGTCTGGAATGGATTGGATACATTATCCTACCAAGTGGTTATACTAATTACA 180
Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct: 181 ATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACA 240
Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294
Sbjct: 241 TGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA 293

Score = 229 (63.3 bits), Expect = 3.1e-100, Sum P(2) = 3.1e-100
Identities = 49/53 (92%), Positives = 49/53 (92%), Strand = Plus / Plus

Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 316 GGGACTATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 368

```

>gb|J00493|MUSIGHAP Mouse Ig active H-chain V-region from 93G7, subgroup VH-II,
mRNA.
Length = 437

Plus Strand HSPs:

```

Score = 1137 (314.2 bits), Expect = 3.2e-100, Sum P(2) = 3.2e-100
Identities = 269/321 (83%), Positives = 269/321 (83%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct: 76 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCCTCAGTGAAGATGT 135
Query: 62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct: 136 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 195
Query: 122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct: 196 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATATTAACTACA 255
Query: 182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct: 256 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 315
Query: 242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
Sbjct: 316 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTCTGTGCAAGATCCCAT 375
Query: 302 GGGAGGGTGCTCTGGACTACT 322
Sbjct: 376 ACTATGGTGGTAGCTACGACT 396

Score = 142 (39.2 bits), Expect = 3.2e-100, Sum P(2) = 3.2e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct: 397 TTGACTACTGGGGCAAGGCACCCCTCTCACAGTCTCCTCA 437

```

>gb|M32035|MUSIGHRI Mouse Ig H-chain mRNA V-D-J region, from hybridoma P65D6-7,
partial cds.
Length = 363

Score = 142 (39.2 bits), Expect = 3.8e-100, Sum P(2) = 3.8e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

Query: 314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 320 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 360

>emb|222088|MDIGGVAR M.domesticus IgG variable region.
Length = 357

Plus Strand HSPs:

Score = 1056 (291.8 bits), Expect = 3.9e-100, Sum P(2) = 3.9e-100
Identities = 248/294 (84%), Positives = 248/294 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAGCTGCAGCAGTCTGAGGGCTGAAGTGGCAAGACCTGGGGCCTCAGTGAAGATG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTTACCAGATACTGGATGCACTGGGTAAACAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCTCTGGAATGGATTGGCGCTATTTATCCTGGAAATAGTGATACTAATAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AACCAGAAATTCAAGGGCAAGGCCAACTGACTGCAGTCACATCTGCCAGCACTGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294

Sbjct: 241 ATGGAACCTCAGCAGCCTGGCATCTGAGGACTCTGCCGTCTATTACTGTGCAAGA 294

Score = 223 (61.6 bits), Expect = 3.9e-100, Sum P(2) = 3.9e-100
Identities = 51/59 (86%), Positives = 51/59 (86%), Strand = Plus / Plus

Query: 296 GGAACCTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 299 GGTACAGGGGATATTCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 357

>gb|M97876|MUSL77IGHV Mouse hybridoma Ig rearranged H-chain mRNA V-region,
partial cds.
Length = 390

Plus Strand HSPs:

Score = 1066 (294.6 bits), Expect = 4.3e-100, Sum P(2) = 4.3e-100
Identities = 246/287 (85%), Positives = 246/287 (85%), Strand = Plus / Plus

Query: 8 ATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCCTGCA 67

Sbjct: 8 ATCTTCAGGAGTCGGGACCTGAGCTGGTGAGGCTGGGGCTTCACTGAAGATGTCCTGCA 67

Query: 68 AGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGAC 127

Sbjct: 68 AGGCTTCTGGATACACATTCACTGACTATGTTATAACCTGGGTGAAGCCGAGAAGTGGAC 127

Query: 128 AGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTACAATCAGA 187

Sbjct: 128 AGGGCCTTGAGTGGATTGGAGAGATTATCCTGGAAGTGGTAGTGCTTACTACAATGAGA 187

Query: 188 AGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGA 247

Sbjct: 188 AGTTCAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAACACAGCCTACATGCAGC 247

Query: 248 TCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGA 294

Sbjct: 248 |||||TCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGA 294

Score = 212 (58.6 bits), Expect = 4.3e-100, Sum P(2) = 4.3e-100
Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 315 |||||TGCCTTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 360

>gb|M61026|MUSIGHAANN M.musculus Ig rearranged H-chain mRNA V-D-J-region,
partial cds.
Length = 354

Plus Strand HSPs:

Score = 1266 (349.8 bits), Expect = 4.4e-100, P = 4.4e-100
Identities = 298/354 (84%), Positives = 298/354 (84%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAGCTTGGAAGCCTGGGGCTTCAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTTGATGCACTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGATATTAC 300

Query: 301 TGGGAGGGTGTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 301 TACGGTGGTGTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

>emb|Z12794|MMV20552B M.musculus mRNA for VH-gen sequence of naturally
occurring, somatically mutated memory B cell
Length = 369

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 253/305 (82%), Positives = 253/305 (82%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAACCTGCAGCAGCCTGGGGCTGAACCTTGGAAGCCTGGGGCTTCAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCACTGGGTAAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

|||||

Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC 300

Query: 301 TGGGA 305

Sbjct: 301 TATGA 305

Score = 221 (61.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 324 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 369

>emb|Z12799|MMV20652B M.musculus mRNA for VH-gen sequence of naturally
occurring, somatically mutated memory B cell
Length = 369

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 253/305 (82%), Positives = 253/305 (82%), Strand = Plus / Plus

Query: 1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCTCAGTGAAGATG 60

Sbjct: 1 CAGGTCCAAGTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTCAGTGAAGCTG 60

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120

Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180

Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240

Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 300

Sbjct: 241 ATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC 300

Query: 301 TGGGA 305

Sbjct: 301 TATGA 305

Score = 221 (61.1 bits), Expect = 4.5e-100, Sum P(2) = 4.5e-100
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 324 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 369

>emb|Z22129|MD1GMVBC M.domesticus IgM variable region.
Length = 363

Plus Strand HSPs:

Score = 1057 (292.1 bits), Expect = 4.6e-100, Sum P(2) = 4.6e-100
Identities = 249/296 (84%), Positives = 249/296 (84%), Strand = Plus / Plus

Query: 2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCTCAGTGAAGATGT 61

```

Sbjct:      2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGT 61
Query:      62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct:      62 CCTGCAAGGCTTCTGGATACACATTCAGTCTAGCTATGTTATGCACTGGGTGAAGCAGAAGC 121
Query:     122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct:     122 CTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTACA 181
Query:     182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct:     182 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241
Query:     242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 297
Sbjct:     242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGAAGG 297

```

Score = 221 (61.1 bits), Expect = 4.6e-100, Sum P(2) = 4.6e-100
Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

```

Query:      309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct:      318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>emb|Z22134|MDIGMVB M.domesticus IgM variable region.
Length = 363

Plus Strand HSPs:

Score = 1063 (293.7 bits), Expect = 8.2e-100, Sum P(2) = 8.2e-100
Identities = 255/308 (82%), Positives = 255/308 (82%), Strand = Plus / Plus

```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAAGTCTGGGGCCTCAGTGAAGATGT 61
Sbjct:      2 AGGTCCAGCTGCAGCAGTCTGGACCTGAGCTGGTAAAGCCTGGGGCTTCAGTGAAGATGT 61
Query:      62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
Sbjct:      62 CCTGCAAGGCTTCTGGATACACATTCAGTCTAGCTATGTTATGCACTGGGTGAAGCAGAAGC 121
Query:     122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
Sbjct:     122 CTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTAAGTACA 181
Query:     182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
Sbjct:     182 ATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACA 241
Query:     242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAGT 301
Sbjct:     242 TGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACTGTGCAAGGGGGGCC 301
Query:      302 GGGAGGGT 309
Sbjct:      302 GGTATGAT 309

```

Score = 212 (58.6 bits), Expect = 8.2e-100, Sum P(2) = 8.2e-100
Identities = 44/46 (95%), Positives = 44/46 (95%), Strand = Plus / Plus

```

Query:      309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
Sbjct:      318 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 363

```

>gb|M64141|MUSIGHNOL Mouse Ig active heavy-chain mRNA V-region.

Length = 339

Plus Strand HSPs:

Score = 1046 (289.0 bits), Expect = 8.8e-100, Sum P(2) = 8.8e-100
Identities = 242/283 (85%), Positives = 242/283 (85%), Strand = Plus / Plus

[illegible]

Score = 229 (63.3 bits), Expect = 8.8e-100, Sum P(2) = 8.8e-100
Identities = 49/53 (92%), Positives = 49/53 (92%), Strand = Plus / Plus

Query: 302 GGGAGGGTCTCTGGACTACTGGGTC AAGGAACCTCAGTCACC GTCTCCTCA 354
 ||| | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 282 GGGGGATGGTATGGACTACTGGGTC AAGGAACCTCAGTCACC GTCTCCTCA 334

>gb|109505|109505 Sequence 3 from patent WO 8909622.
Length = 443

Plus Strand HSPs:

Score = 1107 (305.9 bits), Expect = 9.8e-100, Sum P(2) = 9.8e-100
Identities = 255/297 (85%), Positives = 255/297 (85%), Strand = Plus / Plus

```

Query:      1  CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGCTCTGGGGCCTCAGTGAAGATG  60
             |||||
Sbjct:     95  CAGGTC CAGCTT CAGCAGTCTGGGGCTGAAC TGGCAAACCTGGGGCCTCAGTGAAGATG  154
             |||||

Query:     61  TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCAGCTGGGTAAGCAGACA  120
             |||||
Sbjct:    155  TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCAGCTGGGTA AACAGAGG  214
             |||||

Query:    121  CCTGGACAGGGCCTGGAATGGAATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC  180
             |||||
Sbjct:    215  CCTGGACAGGGTCTGGAATGGAATTGGATATATTAATCCTAGCACTGGGTAT TACTGAATAC  274
             |||||

Query:    181  AATCAGAAGTTTAAAGGCAAGGCCCTATTGACTGCAGACACATCCTCCAGCACAGCCTAC  240
             |||||
Sbjct:    275  AATCAGAAGTTC AAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC  334
             |||||

Query:    241  ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG  297
             |||||
Sbjct:    335  ATGCAACTGAGCAGCCTGACATTTGAGGACTCTGCAGCTTATTACTGTGCAAGAGGG  391
             |||||

```

Score = 166 (45.9 bits), Expect = 9.8e-100, Sum P(2) = 9.8e-100
Identities = 42/53 (79%), Positives = 42/53 (79%), Strand = Plus / Plus

Query: 302 GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354

Sbjct: 390 GGGGGGGGCTCTTTGACTACTGGGGCCAAGGAACCACTCTCACAGTCTCCTCA 442

>gb|M31908|MUSIGHRC Mouse Ig H-chain V-D-J region mRNA, from hybridoma
hVH65-211, partial cds.
Length = 363

Plus Strand HSPs:

Score = 1132 (312.8 bits), Expect = 9.9e-100, Sum P(2) = 9.9e-100
Identities = 264/311 (84%), Positives = 264/311 (84%), Strand = Plus / Plus

```

Query:      2 AGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGT 61
             |||||
Sbjct:      2 AGGTTCAAGCTTCAGCAGTCTGGAGCTGAGCTGGTGAGGGCTGGGTCTCAGTGAAGATGT 61

Query:     62 CCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACAC 121
             |||||
Sbjct:     62 CCTGCAAGGCTTCTGGATATACATTACAAGCTACGGTATAAACTGGGTGAAACAGAGGC 121

Query:    122 CTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTACA 181
             |||||
Sbjct:    122 CTGGACAGGGCCTGGAATGGATTGGATATATTAATCCTGGAAATGGTTATATTAAGTACA 181

Query:    182 ATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACA 241
             |||||
Sbjct:    182 ATGAGAAGTTCAAGGGCAAGACCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACA 241

Query:    242 TGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAAC 301
             |||||
Sbjct:    242 TGCAGCTCAGAAGCCTGACATCTGAGGACTCTGCAGTCTATTTCTGTGCAAGATCGGAAT 301

Query:    302 GGGAGGGTGCT 312
             |||||
Sbjct:    302 ACTATGGTGGT 312

```

Score = 142 (39.2 bits), Expect = 9.9e-100, Sum P(2) = 9.9e-100
Identities = 34/41 (82%), Positives = 34/41 (82%), Strand = Plus / Plus

```

Query:     314 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
             |||||
Sbjct:     323 TTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA 363

```

>gb|M28251|MUSIGHMX Mouse Ig rearranged gamma-chain (G-2a) mRNA V-region
(V-J2), partial cds.
Length = 406

Plus Strand HSPs:

Score = 1107 (305.9 bits), Expect = 1.1e-99, Sum P(2) = 1.1e-99
Identities = 255/297 (85%), Positives = 255/297 (85%), Strand = Plus / Plus

```

Query:      1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG 60
             |||||
Sbjct:     58 CAGGTCCAGCTTCAGCAGTCTGGGGCTGAACTGGCAAACTGGGGCCTCAGTGAAGATG 117

Query:     61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
             |||||
Sbjct:    118 TCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGGTAAACAGAGG 177

Query:    121 CCTGGACAGGGCCTGGAATGGATTGGAAATATTTTCTGGAAATGGTGATACTTACTAC 180
             |||||
Sbjct:    178 CCTGGACAGGGTCTGGAATGGATTGGATATATTAATCCTAGCACTGGGTATACTGAATAC 237

Query:    181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
             |||||
Sbjct:    238 AATCAGAAGTTCAAGGACAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC 297

```

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGG 297
 ||||| | ||||||||| ||| ||||||| ||||||| ||||||| ||||||| |||||||
 Sbjct: 298 ATGCAACTGAGCAGCCTGACATTTGAGGACTCTGCAGTCTATTACTGTGCAAGAGGG 354

Sbjct: 1 CAGGTCCAAGTGCAGCAGCCTGGGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTG 60

11D10 Heavy Chain NUCLEOTIDE - 32

Query: 61 TCCTGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACA 120
 |||||
 Sbjct: 61 TCCTGCAAGGCTTCTGGCTACACCTTACCAGCTACTGGATGCACTGGGTGAAGCAGAGG 120

Query: 121 CCTGGACAGGGCCTGGAATGGATTGGAATATTTTCTGGAAATGGTGATACTTACTAC 180
 |||||
 Sbjct: 121 CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTGATCCTAATAGTGGTGGTACTAAGTAC 180

Query: 181 AATCAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTAC 240
 |||||
 Sbjct: 181 AATGAGAAGTTCAAGAGCAAGGCCACACTGACTGTAGACAAACCTCCAGCACAGCCTAC 240

Query: 241 ATGCAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTCTGTGCAAGAGGGAAC 300
 |||||
 Sbjct: 241 ATGCAGCTCAGCAGCCTGACACCTGAGGACTCTGCGGTCTATTATTGTGCAAGAGACTAC 300

Query: 301 TGGGA 305
 ||
 Sbjct: 301 TATGA 305

Score = 221 (61.1 bits), Expect = 2.5e-99, Sum P(2) = 2.5e-99
 Identities = 45/46 (97%), Positives = 45/46 (97%), Strand = Plus / Plus

Query: 309 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 354
 |||||
 Sbjct: 324 TGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 369

WARNING: HSPs involving 4964 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100
 B=50
 H=1
 -qtype
 E=10

-ctxfactor=2.00

Query	Strand	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+1	0	+5,-4	0.192	0.173	0.357	same	same	same	
-1	0	+5,-4	0.192	0.173	0.357	same	same	same	

Query	Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+1	0	0	354	354	10.117	11	N/A	73	0.025	76	
-1	0	0	354	354	10.117	11	N/A	73	0.025	76	

Statistics:

Query	Strand	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+1	0	0	124 (34.3 bits)	1473 (407.0 bits)	6865	93
-1	0	0	124 (34.3 bits)	1065 (294.3 bits)	31	0

Query	Strand	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+1	0	0	347	86244	31541	44804	9985	378
-1	0	0	347	48074	4289	42064	1816	1

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL

Release date: 6:31 AM EST Jan 19, 1996

Posted date: 6:39 AM EST Jan 19, 1996

of letters in database: 449,479,361

of sequences in database: 662,343

of database sequences satisfying E: 5014

No. of states in DFA: 204 (204 KB)

Total size of DFA: 213 KB (256 KB)
Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 3
Time to search database: 30.08u 3.42s 33.50t Real: 00:01:10
Total cpu time: 30.22u 3.54s 33.76t Real: 00:01:11

WARNINGS ISSUED: 2

S. Chatterjee

===== 1382

Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>

Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTMP id 2504; Fri, 19 Jan 1996 17:18:47 -0500

Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP; Fri, 19 Jan 96 17:18:44 EST

Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov id RAA28107; Fri, 19 Jan 1996 17:18:34 -0500

Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6) id RAA05609; Fri, 19 Jan 1996 17:18:33 -0500

Date: Fri, 19 Jan 1996 17:18:33 -0500

Message-Id: <199601192218.RAA05609@blaster.nlm.nih.gov>

To: SKCHAT00@UKCC.uky.edu

Subject: Results-BLAST Server

From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>

Errors-To: <owner-blast@ncbi.nlm.nih.gov>

Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov' with the word HELP in the body of the message. The documentation was last modified March 18th.

March 18, 1995

The BLAST FAQ was updated with the question Q33 related to degenerated nucleotide code available for the BLAST programs.

August 8, 1995

A new server directive ACKNOWLEDGE, has been added to the server. See the help file for more details.

Trying blaster... connected

National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:17:34 EST 1996, Up 30 days, 5:08, 1 user, load: 62.31, 41.55, 28.47

PEPTIDE SEQUENCE DATABASES

nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUpdate, updated daily for efficient, complete searches of the five component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release
swissprot SWISS-PROT Release 32.0, December 1995
pir PIR Release 45.0 (complete), June 30, 1995
spupdate SWISS-PROT cumulative weekly update to the major release
genpept CDS translations from GenBank(R) Release 92, December 15, 1995
gpupdate cumulative daily updates to the major release of genpept
kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995
tfd TFD transcription factor (protein) database Release 7.0, June 1993
alu * Translations of select Alu repeats from REPBASE

NUCLEOTIDE SEQUENCE DATABASES

nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily for efficient, complete searches of the four component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release
genbank GenBank(R) Release 92 (no daily updates), December 15, 1995
gbupdate GenBank(R) cumulative daily updates to the major release
embl EMBL Data Library, Release 45.0, December 1995
emblu EMBL Data Library cumulative daily updates to the major release
vector Vector subset of GenBank(R), February 3rd, 1995
alu ** Select Alu repeats from REPBASE
kabatnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
epd Eukaryotic Promoter Database Release 43, June 1995
dbest + Database of Expressed Sequence Tags (cumulative daily update)
dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994

* Databases that are not accessible through the NCBI Retrieve E-mail server.
+ The TBLASTX program is restricted to searching these databases.

You can obtain the BLAST documentation files, send a message consisting of just the word "help" (without the quotes) to: blast@ncbi.nlm.nih.gov
Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov/>

BLASTP 1.4.8MP [20-June-1995] [Build 13:58:02 Oct 17 1995]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Query= 11D10VH.pep
(118 letters)

Database: Non-redundant PDB+SwissProt+SPupdate+PIR+GenPept+GPupdate
172,206 sequences; 51,001,589 total letters.

```
Searching.....done
```

Observed Numbers of Database Sequences Satisfying Various EXPECTation Thresholds (E parameter values)

Histogram units: = 39 Sequences : less than 39 sequences

EXPECTation Threshold
(E parameter)

[illegible]

0.016	6047	117	===
0.010	5930	75	=
0.0063	5855	98	==
0.0040	5757	112	==
0.0025	5645	104	==
0.0016	5541	72	=

Sequences producing High-scoring Segment Pairs:			High	Smallest Sum	Probability	
			Score	P(N)	N	
gp	X64805	MMA1DHCH_1	anti-Id mAb 114 haevy chain, V-reg...	542	7.4e-70	1
gp	M17953	MUSIGHXW_1	immunoglobulin heavy chain [Mus mu...	462	4.2e-65	2
gp	Z22117	MDIGGVBC_1	immunoglobulin variable region [Mu...	430	2.3e-64	2
gp	U10410	MMU10410_1	antineuraminidase single chain ant...	425	1.3e-63	2
pir	S38950	S38950	Ig gamma chain - mouse	420	2.6e-63	2
gp	Z22034	MDIGGVAG_1	immunoglobulin variable region [Mu...	421	4.0e-63	2
gp	U40581	MMU40581_1	sFv antibody [Mus musculus]	409	1.1e-61	2
gp	A13735	A13735_1	V region monoclonal antibody,cross...	390	1.3e-61	2
pir	PS0024	PS0024	Ig heavy chain precursor V region ...	390	1.5e-61	2
gp	Z22059	MDIGGVAN_1	immunoglobulin variable region [Mu...	417	1.7e-61	2
pir	E48677	E48677	Ig heavy chain V-D-J region (48) -...	404	3.1e-61	2
gp	M32037	MUSIGHRK_1	Mouse Ig H-chain mRNA V-D-J region...	419	3.1e-61	2
pir	S41394	S41394	Ig heavy chain V region - mouse	407	8.1e-61	2
gp	S69279	S69279_1	anti-louping ill virus antibody 4....	405	8.1e-61	2
gp	Z22088	MDIGGVAR_1	immunoglobulin variable region [Mu...	407	8.1e-61	2
pir	F48677	F48677	Ig heavy chain V-D-J region (44.1)...	400	1.1e-60	2
gp	L22747	MUSF_1	immunoglobulin heavy chain [Mus mu...	475	1.1e-60	1
gp	M32036	MUSIGHRJ_1	Mouse Ig H-chain mRNA V-D-J region...	414	1.5e-60	2
pir	A26405	A26405	Ig heavy chain V region (3D10) - m...	400	1.5e-60	2
gp	U26991	MMU26991_1	Ig variable region [Mus musculus]	473	1.8e-60	1
pir	PL0208	PL0208	anti-idiotypic antibody E225, gamm...	418	1.8e-60	2
gp	X53637	MME225H_1	E225 gene product [Mus musculus]	418	1.8e-60	2
gp	M34581	MUSIGHABU_1	Mouse Ig heavy-chain mRNA V-D-J re...	408	2.0e-60	2
gp	L24557	MUSIGHADQ_1	immunoglobulin heavy chain [Mus mu...	401	2.0e-60	2
gp	M36210	MUSIGHADQ_1	immunoglobulin heavy chain V-regio...	422	2.1e-60	2
gp	M28251	MUSIGHMX_1	Mouse Ig rearranged gamma-chain (G...	406	2.5e-60	2
gp	Z22129	MDIGMVBC_1	immunoglobulin variable region [Mu...	400	2.8e-60	2
pir	S26309	S26309	Ig heavy chain V region - mouse	394	2.9e-60	2
gp	M32035	MUSIGHRI_1	Mouse Ig H-chain mRNA V-D-J region...	411	3.8e-60	2
gp	S74051	S74051_1	Ig VH gene product [Mus sp.]	471	4.0e-60	1
pir	PH1482	PH1482	Ig heavy chain V region (clones 36...	410	4.5e-60	2
gp	X06110	MMIGVHD1_1	Mouse mRNA (36-35) for immunoglobu...	410	5.2e-60	2
gp	Z22134	MDIGMVBF_1	immunoglobulin variable region [Mu...	401	5.2e-60	2
gp	K00684	MUSIGHBG_1	Mouse Ig active H-chain V-region f...	409	6.2e-60	2
sp	P01747	HV03_MOUSE	IG HEAVY CHAIN V REGION (36-65).	409	7.2e-60	2
pir	B22769	B22769	Ig heavy chain V region (B1-8.V1/V...	409	7.2e-60	2
gp	M36216	MUSIGHADW_1	immunoglobulin heavy chain V-regio...	409	7.2e-60	2
gp	L25855	MUSIGGB_1	IgG gene product [Mus musculus]	407	7.3e-60	2
gp	S77022	S77022_1	anti-CD29 antibody heavy chain var...	403	7.5e-60	2
gp	M36225	MUSIGHAEF_1	immunoglobulin heavy chain V-regio...	468	9.9e-60	1
pir	S40295	S40295	Ig gamma-2a chain (mAb735) - mouse	420	1.1e-59	2
gp	L22749	MUSI_1	immunoglobulin heavy chain [Mus mu...	467	1.4e-59	1
gp	M61026	MUSIGHAANN_1	immunoglobulin heavy chain VDJ reg...	467	1.4e-59	1
gp	M31287	MUSIGHAVA_1	IgG gene product [Mus musculus]	466	1.9e-59	1
gp	M31288	MUSIGHAWA_1	Mouse active rheumatoid factor IgA...	466	1.9e-59	1
gp	M31908	MUSIGHRC_1	Mouse Ig H-chain V-D-J region mRNA...	404	2.5e-59	2
gp	M36226	MUSIGHAEG_1	immunoglobulin heavy chain V-regio...	414	2.5e-59	2
gp	U36491	MMU36491_1	J558+ IgM heavy chain [Mus musculus]	402	2.8e-59	2
gp	L35315	MUSIVDJA_1	immunoglobulin heavy chain [Mus mu...	404	2.9e-59	2
gp	X88902	MMVARHECH_1	Fv fragment variable heavy chain [...	389	3.2e-59	2
gp	M36209	MUSIGHADP_1	immunoglobulin heavy chain V-regio...	415	3.4e-59	2
gp	M12809	MUSIGHJA_1	Mouse Ig rearranged H-chain V-regi...	403	3.4e-59	2
gp	X75095	MMHCVR1_1	ASW1 heavy chain variable regions...	404	3.5e-59	2
gp	M36224	MUSIGHAEE_1	immunoglobulin heavy chain V-regio...	464	3.5e-59	1
pir	A54378	A54378	anti-triplex DNA immunoglobulin he...	464	3.6e-59	1
sp	P01746	HV02_MOUSE	IG HEAVY CHAIN PRECURSOR V REGION ...	405	4.0e-59	2

pir S21810 S21810	Ig heavy chain V region - mouse >g...	410	4.1e-59	2
gp M33856 MUSIGHABM_1	Mouse Ig H-chain mRNA V-region, 5'...	403	4.2e-59	2
pir G48677 G48677	Ig heavy chain V-D-J region (419.1...	388	4.6e-59	2
gp Z22028 MDIGGVAD_1	Immunoglobulin Variable Region [Mu...	396	4.7e-59	2
gp Z22101 MDIGGVAV_1	immunoglobulin variable region [Mu...	399	4.8e-59	2
pdb 1FBI H	Fab Fragment Of The Monoclonal Ant...	383	6.6e-59	2
gp M31913 MUSIGHRE_1	Mouse Ig H-chain V-D-J region mRNA...	404	8.8e-59	2
gp U39781 MMU39781_1	J558+ IgM heavy chain [Mus musculus]	389	9.4e-59	2
gp M83098 MUSIGHM195_1	immunoglobulin heavy chain [Mus mu...	388	1.1e-58	2
gp M94153 MUSIGKXE_1	immunoglobulin gamma-chain [Mus mu...	400	1.1e-58	2
gp U00927 U00927_1	antibody heavy chain FAB [Mus musc...	386	1.2e-58	2
gp J04548 MUSIGHVBE_1	immunoglobulin gamma-chain [Mus mu...	399	1.4e-58	2
pir PH1489 PH1489	Ig heavy chain V region (clone X41...	399	1.4e-58	2
gp M36213 MUSIGHADT_1	immunoglobulin heavy chain V-regio...	410	1.7e-58	2
gp M36219 MUSIGHADZ_1	immunoglobulin heavy chain V-regio...	404	1.7e-58	2
gp L22746 MUSE_1	immunoglobulin heavy chain [Mus mu...	408	1.7e-58	2
gp M64141 MUSIGHNOL_1	Ig heavy chain [Mus musculus]	391	1.8e-58	2
gp X65773 MLB4IHEV_1	IgE antibody heavy chain (VDJ) [Mu...	458	2.0e-58	1
pir A30577 A30577	Ig heavy chain precursor V region ...	402	2.7e-58	2
pir S31930 S31930	Ig gamma chain - Mouse (fragment) ...	385	2.9e-58	2
pir S20646 S20646	Ig heavy chain V region - mouse >g...	385	3.0e-58	2
gp M36207 MUSIGHAFR_1	immunoglobulin heavy chain V-regio...	408	3.1e-58	2
gp Z22099 MDIGGVAV_1	immunoglobulin variable region [Mu...	397	3.1e-58	2
gp U23046 MMU23046_1	anti-ds-DNA immunoglobulin heavy c...	385	3.1e-58	2
gp L41877 MUSIHCB_1	immunoglobulin heavy chain [Mus mu...	407	3.7e-58	2
gp U22903 MMU22903_1	IgG Vh region [Mus musculus]	393	4.0e-58	2
pir A21854 A21854	Ig heavy chain V region (IF6) - mouse	382	4.2e-58	2
gp M31281 MUSIGHAPAA_1	Mouse active rheumatoid factor IgA...	392	4.3e-58	2
gp J04547 MUSIGHVBD_1	immunoglobulin gamma-chain [Mus mu...	394	4.8e-58	2
pir S20643 S20643	Ig heavy chain V region - mouse >g...	387	5.7e-58	2
pir S25175 S25175	Ig heavy chain V region - mouse >g...	399	5.8e-58	2
pir A24672 A24672	Ig heavy chain precursor V region ...	395	5.8e-58	2
gp M60237 MUSIGHP111_1	immunoglobulin heavy chain [Mus mu...	455	5.9e-58	1
gp X82581 MMIGPE2_1	IgG heavy chain [Mus musculus]	389	6.0e-58	2
gp U07214 MMU07214_1	anti-C5a Ig heavy chain V region [...	455	6.1e-58	1
gp M64134 MUSIGHNOE_1	Ig heavy chain [Mus musculus]	395	6.1e-58	2
gp M64142 MUSIGHNOM_1	Ig heavy chain [Mus musculus]	395	6.2e-58	2
gp S71019 S71019_1	anti-erbB-2 product monoclonal ant...	394	6.4e-58	2
sp P01751 HV07_MOUSE	IG HEAVY CHAIN PRECURSOR V REGION ...	394	6.8e-58	2
gp U26992 MMU26992_1	Ig variable region [Mus musculus]	382	6.9e-58	2
gp M28529 MUSIGHMO_1	Mouse active Ig mu-chain VJ3-regio...	282	7.8e-58	3
pir A22769 A22769	Ig heavy chain V region (B1-8) - m...	394	7.9e-58	2
gp M26808 MUSIGHADM_1	Mouse Ig heavy chain mRNA V-region...	394	7.9e-58	2
gp Z22024 MDIGMVAA_1	immunoglobulin variable region [Mu...	403	8.3e-58	2

WARNING: Descriptions of 8535 database sequences were not reported due to the limiting value of parameter V = 100.

>gp|X64805|MMAIDHCH_1 anti-Id mAb 114 haevy chain, V-region [Mus musculus]
Length = 118

Score = 542 (246.4 bits), Expect = 7.4e-70, P = 7.4e-70
Identities = 100/118 (84%), Positives = 110/118 (93%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPQGQLEWIGNIFPGNGDTYY 60
QAYLQQSGAELVR G+SVKMSCKASGYT TSYNMHWVKQTP QGLEWIG I+PGNGDT Y
Sbjct: 1 QAYLQQSGAELVRPGSSVKMSCKASGYFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSVTVSS 118
NQKFKGKA+LT D SSSTAYMQ+SSLTSEDSAVYFCARG++ G++DYWGQGT++TVSS
Sbjct: 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARGDYSIDYWGQGTTLTVSS 118

>gp|M17953|MUSIGHXW_1 immunoglobulin heavy chain [Mus musculus]
Length = 140

Score = 462 (210.0 bits), Expect = 4.2e-65, Sum P(2) = 4.2e-65
Identities = 88/98 (89%), Positives = 91/98 (92%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
QAYLQQSGAELVR GASVKMSCKASGYT TSYNMHWVKQTP QGLEWIG I+PGNGDT Y
Sbjct: 20 QAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98
NQKFKGKA+LT D SSSTAYMQ+SSLTSEDSAVYFCAR
Sbjct: 80 NQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCAR 117

Score = 50 (22.7 bits), Expect = 4.2e-65, Sum P(2) = 4.2e-65
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 106 DYWGQGTSTVTS 117
D WG GT+VTVS
Sbjct: 129 DVWGTGTTVTVS 140

>gp|Z22117|MDIGGVBC_1 immunoglobulin variable region [Mus musculus domesticus]
Length = 120

Score = 430 (195.5 bits), Expect = 2.3e-64, Sum P(2) = 2.3e-64
Identities = 80/98 (81%), Positives = 88/98 (89%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
+ LQQSG ELV+ GASVK+SCKASGYT T Y MHWVKQ PGQGLEWIG I+PG+G+TTY
Sbjct: 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMHVVKQKPGQGLEWIGEIYPGSGNTYY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98
N+KFKGKASLTAD SSSTAYMQ+SSLTSEDSAVYFCAR
Sbjct: 61 NEKFKGKASLTADKSSSTAYMQLSSLTSEDSAVYFCAR 98

Score = 77 (35.0 bits), Expect = 2.3e-64, Sum P(2) = 2.3e-64
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTS 118
A+DYWGQGTSTVTS
Sbjct: 106 AMDYWGGTSTVTS 120

>gp|U10410|MMU10410_1 antineuraminidase single chain antibody [Mus musculus]
Length = 273

Score = 425 (193.2 bits), Expect = 1.3e-63, Sum P(2) = 1.3e-63
Identities = 79/98 (80%), Positives = 89/98 (90%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAELV+ GASV+MSCKASGYT T+YNM+VVKQ+PGQGLEWIG +PGNGDT Y
Sbjct: 23 QVQLQQSGAELVKPGASVMSCKASGYTFTNYNMYVVKQSPGGGLEWIGIFYPGNGDTSY 82

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98
NQKFK KA+LTAD SS+TAYMQ+SSLTSEDSAVY+CAR
Sbjct: 83 NQKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYFCAR 120

Score = 74 (33.6 bits), Expect = 1.3e-63, Sum P(2) = 1.3e-63
Identities = 12/17 (70%), Positives = 15/17 (88%)

Query: 101 WEGALDYWGQGTSTVTS 117
++G DYWGQGT+VTVS
Sbjct: 127 YDGGFDYWGGTSTVTS 143

>pir|S38950|S38950 Ig gamma chain - mouse
Length = 246

Score = 420 (190.9 bits), Expect = 2.6e-63, Sum P(2) = 2.6e-63
Identities = 79/99 (79%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELVR GASVK+SCKASGYT T Y +HWVKQ PG+GLEWIG I+PG+G+T Y
 Sbjct: 1 QIQLQQSGPELVKPGASVKISCKASGYTFTDYYIHWVKQRPGEGLWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARG 99
 N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 77 (35.0 bits), Expect = 2.6e-63, Sum P(2) = 2.6e-63
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 103 AMDYWGQGTSTVTVSS 117

>gp|Z22034|MDIGGVAG_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 119

Score = 421 (191.4 bits), Expect = 4.0e-63, Sum P(2) = 4.0e-63
 Identities = 79/104 (75%), Positives = 90/104 (86%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELV+ GASVK+SCKASGYT T Y +HWVKQ+PGQGLEWIG I+PG+G+T Y
 Sbjct: 1 QVQLQQSGPELVKPGASVKLSCKASGYTFTDYYIHWVKQSPGQGLEWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGNWEA 104
 N KFKGKA++TAD SSSTAYMQ+SSLTSEDSAVYFCARG G+
 Sbjct: 61 NDKFKGKATMTADKSSSTAYMQLSSLTSEDSAVYFCARGVARG 104

Score = 77 (35.0 bits), Expect = 4.0e-63, Sum P(2) = 4.0e-63
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 105 AMDYWGQGTSTVTVSS 119

>gp|U40581|MMU40581_1 sFv antibody [Mus musculus]
 Length = 246

Score = 409 (185.9 bits), Expect = 1.1e-61, Sum P(2) = 1.1e-61
 Identities = 78/99 (78%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQ+SGAELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIG I P NG T Y
 Sbjct: 1 QVQLQESGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGEGLWIGKINPSNGRTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARG 99
 N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CARG
 Sbjct: 61 NEKFKKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 76 (34.5 bits), Expect = 1.1e-61, Sum P(2) = 1.1e-61
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 ALDYWGQGT+VTVSS
 Sbjct: 109 ALDYWGQGT+VTVSS 123

Score = 50 (22.7 bits), Expect = 0.0083, Sum P(3) = 0.0083
 Identities = 8/20 (40%), Positives = 14/20 (70%)

Query: 81 MQISLTSEDSAVYFCARGN 100
 + I+S+ +ED +YFC + N
 Sbjct: 211 LSINSVETEDFGMYFCQQSN 230

Score = 39 (17.7 bits), Expect = 0.0083, Sum P(3) = 0.0083
 Identities = 8/14 (57%), Positives = 10/14 (71%)

Query: 12 VRSGASVKMSCKAS 25
V G SV +SC+AS
Sbjct: 151 VTPGDSVSLSCRAS 164

Score = 34 (15.5 bits), Expect = 0.0083, Sum P(3) = 0.0083
Identities = 5/9 (55%), Positives = 7/9 (77%)

Query: 31 SYNMHVVKQ 39
S N+HW +Q
Sbjct: 168 SNNLHWYQQ 176

>gp|A13735|A13735_1 V region monoclonal antibody, cross reacts with 19 known
P.aeruginosa serotypes [unidentified] >gp|M28834|MUSIGHALPA_1
immunoglobulin gamma-2a chain [Mus musculus]
Length = 159

Score = 390 (177.3 bits), Expect = 1.3e-61, Sum P(2) = 1.3e-61
Identities = 76/98 (77%), Positives = 81/98 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT T+Y MHVVKQ PGQGLEWIG I P G T Y
Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTAYWMHVVKQRPQGLEWIGYINPNTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 98
NQ FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+C R
Sbjct: 80 NQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCTR 117

Score = 96 (43.6 bits), Expect = 1.3e-61, Sum P(2) = 1.3e-61
Identities = 17/19 (89%), Positives = 19/19 (100%)

Query: 100 NWEALDYWGQGSTVTVSS 118
N+EGA+DYWGQGSTVTVSS
Sbjct: 121 NYEGAMDYWGQGSTVTVSS 139

>pir|PS0024|PS0024 Ig heavy chain precursor V region (6A4) - mouse
Length = 139

Score = 390 (177.3 bits), Expect = 1.5e-61, Sum P(2) = 1.5e-61
Identities = 76/98 (77%), Positives = 81/98 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT T+Y MHVVKQ PGQGLEWIG I P G T Y
Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTAYWMHVVKQRPQGLEWIGYINPNTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 98
NQ FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+C R
Sbjct: 80 NQNFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCTR 117

Score = 96 (43.6 bits), Expect = 1.5e-61, Sum P(2) = 1.5e-61
Identities = 17/19 (89%), Positives = 19/19 (100%)

Query: 100 NWEALDYWGQGSTVTVSS 118
N+EGA+DYWGQGSTVTVSS
Sbjct: 121 NYEGAMDYWGQGSTVTVSS 139

>gp|Z22059|MDIGGVAN_1 immunoglobulin variable region [Mus musculus domesticus]
Length = 121

Score = 417 (189.6 bits), Expect = 1.7e-61, Sum P(2) = 1.7e-61
Identities = 79/100 (79%), Positives = 89/100 (89%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSG ELVR GASVK+SCKASGYT T Y ++VVKQ PGQGLEWIG I+PG+G+T Y
Sbjct: 1 QIQLQQSGPELVPRGASVKISCKASGYTFTDYYINWVKQRPQGLEWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGN 100

N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG+
 Sbjct: 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGD 100

Score = 69 (31.4 bits), Expect = 1.7e-61, Sum P(2) = 1.7e-61
 Identities = 12/14 (85%), Positives = 14/14 (100%)

Query: 105 LDYWGQGTSTVSS 118
 LDYWGQGT++TVSS
 Sbjct: 108 LDYWGQGTTLTVSS 121

>pir|E48677|E48677 Ig heavy chain V-D-J region (48) - mouse (fragment)
 Length = 123

Score = 404 (183.7 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 78/108 (72%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
 Sbjct: 1 QVRLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNVVKQRPQGLEWIGYINPGNGYINY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAV+FCAR ++ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFFCARSSYFGGGYYY 108

Score = 80 (36.4 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 15/20 (75%), Positives = 17/20 (85%)

Query: 99 GNWEALDYWGQGTSTVSS 118
 G + A+DYWGQGTSTVSS
 Sbjct: 104 GGGYYAMDYWGQGTSTVSS 123

>gp|M32037|MUSIGHRK_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
 P6514-2, partial cds. [Mus musculus] >gp|M32038|MUSIGHRL_1 Mouse Ig
 H-chain mRNA V-D-J region, from hybridoma P65J4-1, partial cds.
 [Mus musculus]
 Length = 121

Score = 419 (190.5 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 80/108 (74%), Positives = 90/108 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
 Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR N+ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSNYGGSYFF 108

Score = 65 (29.5 bits), Expect = 3.1e-61, Sum P(2) = 3.1e-61
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVSS 118
 DYWGQGT++TVSS
 Sbjct: 109 DYWGQGTTLTVSS 121

>pir|S41394|S41394 Ig heavy chain V region - mouse
 Length = 120

Score = 407 (185.0 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 78/98 (79%), Positives = 84/98 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELV+ GASVK+SCKASGYT TSY MHVVKQ PGQGLEWIG I P + TYY
 Sbjct: 1 EVQLQQSGAELVKPGASVKLSCKASGYTFTSYMMHVVKQRPQGLEWIGEIDPSDSYTTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 98

NQKFKGKA+LT D SSSTAYMQ SSLTSEDSAVY+CAR
 Sbjct: 61 NQKFKGKATLTVDKSSSTAYMQSSLTSEDSAVYYCAR 98

Score = 74 (33.6 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ++DYWGQGTSTVTSS
 Sbjct: 106 SMDYWGGGTSTVTSS 120

>gp|S69279|S69279_1 anti-louping ill virus antibody 4.2 heavy-chain variable
 region [Mus sp.]
 Length = 120

Score = 405 (184.1 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 77/99 (77%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSG ELV+ GASVKMSCKASGYT T Y + WVKQ GQGLEWIG I+PG+G TYY
 Sbjct: 1 QVQLQQSGPELVKPGASVKMSCKASGYTFDYVIGWVKQRTGQGLEWIGEIYPGSGTYY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG 99
 N+KFK KA+LTAD SS+TAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYFCARG 99

Score = 76 (34.5 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ALDYWGQGT+VTSS
 Sbjct: 106 ALDYWGQGT+VTSS 120

>gp|Z22088|MDIGGVAR_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 119

Score = 407 (185.0 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 78/103 (75%), Positives = 84/103 (81%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQS AEL R GASVKMSCKASGYT T Y MHWVKQ PGQ LEWIG I+PGN DT Y
 Sbjct: 1 QVQLQQSEAEARPGASVKMSCKASGYTFTRYMMHWVKQRPQGLEWIGAIYPGNSDTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEG 103
 NQKFKGKA LTA TS+STAYM++SSL SEDSAVY+CAR + G
 Sbjct: 61 NQKFKGKALTAVTSASTAYMELSSLASEDSAVYFCARSRYRG 103

Score = 74 (33.6 bits), Expect = 8.1e-61, Sum P(2) = 8.1e-61
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 ++DYWGQGTSTVTSS
 Sbjct: 105 SMDYWGGGTSTVTSS 119

>pir|F48677|F48677 Ig heavy chain V-D-J region (44.1) - mouse (fragment)
 Length = 123

Score = 400 (181.8 bits), Expect = 1.1e-60, Sum P(2) = 1.1e-60
 Identities = 77/108 (71%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR+G+SVK+SCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
 Sbjct: 1 QVRLQQSGAELVRAGSSVKISCKASGYTFTSYGVNHWKQRPQGLEWIGYINPGNGYIKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAV+FCAR ++ G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVFFCARSSYFGGGYY 108

Score = 80 (36.4 bits), Expect = 1.1e-60, Sum P(2) = 1.1e-60
Identities = 15/20 (75%), Positives = 17/20 (85%)

Query: 99 GNWEGALDYWGQGSTVTVSS 118
G + A+DYWGQGSTVTVSS
Sbjct: 104 GGYYYAMDYWGQGSTVTVSS 123

>gp|L22747|MUSF_1 immunoglobulin heavy chain [Mus musculus]
Length = 118

Score = 475 (215.9 bits), Expect = 1.1e-60, P = 1.1e-60
Identities = 90/118 (76%), Positives = 103/118 (87%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKRPGHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGNWEALDYWGQGSTVTVSS 118
N+KFKGKA+LTADTSSSTAYMQ+SLTSEDSAVYFCAR ++ G+ DYWGQGT++TVSS
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSLTSEDSAVYFCARPHYGGSDYWGQGTTLTVSS 118

>gp|M32036|MUSIGHRJ_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
P65D6-3, partial cds. [Mus musculus]
Length = 121

Score = 414 (188.2 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 79/108 (73%), Positives = 90/108 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKRPGQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGNWEALDYW 108
N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR ++ G Y+
Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYYF 108

Score = 65 (29.5 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGSTVTVSS 118
DYWGQGT++TVSS
Sbjct: 109 DYWGQGTTLTVSS 121

>pir|A26405|A26405 Ig heavy chain V region (3D10) - mouse
Length = 121

Score = 400 (181.8 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 75/103 (72%), Positives = 86/103 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG ELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y
Sbjct: 1 EVQLQQSGTELVRAGSSVKMSCKASGYTFTSYGINWVKRPGQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGNWE 103
N+KFKGK +LT D SSSTAYMQ+ SLTSED+AVYFC+R + G
Sbjct: 61 NEKFKGKTTLTVDRSSSTAYMQLRSLTSEDAAVYFCRSEYYG 103

Score = 79 (35.9 bits), Expect = 1.5e-60, Sum P(2) = 1.5e-60
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGSTVTVSS 118
ALDYWGQGSTVTVSS
Sbjct: 107 ALDYWGQGSTVTVSS 121

11D10 Heavy Chain PEPTIDE - 11

>gp|U26991|MMU26991_1 Ig variable region [Mus musculus]
Length = 137

Score = 473 (215.0 bits), Expect = 1.8e-60, P = 1.8e-60
Identities = 90/118 (76%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
+ LQQSG ELV+ GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P N T Y
Sbjct: 20 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTVSS 118
N+KFKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CAR W +DYWGQGTSTVTVSS
Sbjct: 80 NEKFKGKATLTSKSSSTAYMELSSLTSEDSAVYYCARNGLPPMDYWGQGTSTVTVSS 137

>pir|PL0208|PL0208 anti-idiotypic antibody E225, gamma chain V region - mouse
(strain BALB/c) (fragment)
Length = 136

Score = 418 (190.0 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 77/99 (77%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ G+ELVR GASVK+SCKASGYT T+Y MHWVKQ PGQGLEWIGNI+PG+GD+ Y
Sbjct: 20 QVQLQQPGSELVRPGASVKLSCKASGYTFTNYMHWVKQRPQGLEWIGNIYPGSGDSNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
++KFK KA+LT DTSSSTAYMQ+S LTSEDSAVY+CARG
Sbjct: 80 DEKFKSKATLTVDTSSTAYMQLSGLTSEDSAVYYCARG 118

Score = 60 (27.3 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 10/13 (76%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
D+WGQGT++TVSS
Sbjct: 124 DHWGQGTTLTVSS 136

>gp|X53637|MME225H_1 E225 gene product [Mus musculus]
Length = 136

Score = 418 (190.0 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 77/99 (77%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQ G+ELVR GASVK+SCKASGYT T+Y MHWVKQ PGQGLEWIGNI+PG+GD+ Y
Sbjct: 20 QVQLQQPGSELVRPGASVKLSCKASGYTFTTYMHWVKQRPQGLEWIGNIYPGSGDSNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
++KFK KA+LT DTSSSTAYMQ+S LTSEDSAVY+CARG
Sbjct: 80 DEKFKSKATLTVDTSSTAYMQLSGLTSEDSAVYYCARG 118

Score = 60 (27.3 bits), Expect = 1.8e-60, Sum P(2) = 1.8e-60
Identities = 10/13 (76%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
D+WGQGT++TVSS
Sbjct: 124 DHWGQGTTLTVSS 136

>gp|M34581|MUSIGHABU_1 Mouse Ig heavy-chain mRNA V-D-J region, partial cds.
[Mus musculus] >gp|M31956|MUSIGHRO_1 Mouse Ig active mu-chain mRNA
V-D-J2 region, from hybridoma CH12, partial cds. [Mus musculus]
Length = 122

Score = 408 (185.5 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 78/108 (72%), Positives = 87/108 (80%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60

11D10 Heavy Chain PEPTIDE – 12

Q LQQ G ELV+ GASVK+SCKASGYT TSY MHVVK PGQGLEWIGNI P NG T Y
Sbjct: 1 QVQLQQPGTELVKPGASVKLSCKASGYTFTSYMHVVKQRPQGQLEWIGNINPSNGGTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGNWEALDYW 108
N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR + + Y+

Sbjct: 61 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARDYGGSWGY 108

Score = 70 (31.8 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 12/19 (63%), Positives = 15/19 (78%)

Query: 100 NWEALDYWGQGTSTVSS 118
+W DYWGQGT++TVSS

Sbjct: 104 SWGYFDYWGQGTTLTVSS 122

>gp|L24557|MUSIGHMADQ_1 immunoglobulin heavy chain [Mus musculus]
Length = 122

Score = 401 (182.3 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 76/98 (77%), Positives = 85/98 (86%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYYNQK 63
LQ+SGAEL R GASVKMSCKASGYT + Y+MHVVK PGQGLEWIG I+P +G T YNQK

Sbjct: 3 LQESGAELARPGASVKMSCKASGYTFSRYSMHVVKQRPQGQLEWIGIYPTSGYTNYNQK 62

Query: 64 FKFKASLTADTSSSTAYMQISLTSEDSAVYFCARGN 101
FK KA+LTAD SSSTAYMQ+SSLTSEDSAVY+CAR +

Sbjct: 63 FKDKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSEY 100

Score = 77 (35.0 bits), Expect = 2.0e-60, Sum P(2) = 2.0e-60
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVSS 118
A+DYWGQGTSTVSS

Sbjct: 108 AMDYWGQGTSTVSS 122

>gp|M36210|MUSIGHADQ_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 119

Score = 422 (191.8 bits), Expect = 2.1e-60, Sum P(2) = 2.1e-60
Identities = 80/101 (79%), Positives = 89/101 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVK+SCKASGYT T+Y + VVK PG GLEWIG+I+PG G T Y

Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGVVKQRPQGHLEWIGDIYPGGYTN 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSEDSAVYFCARGN 101
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCARGN+

Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARGN 101

Score = 56 (25.5 bits), Expect = 2.1e-60, Sum P(2) = 2.1e-60
Identities = 10/12 (83%), Positives = 11/12 (91%)

Query: 107 YWGQGTSTVSS 118
YWGQGT VTVS+

Sbjct: 108 YWGQGTTLTVSA 119

>gp|M28251|MUSIGHMX_1 Mouse Ig rearranged gamma-chain (G-2a) mRNA V-region
(V-J2), partial cds. [Mus musculus]
Length = 136

Score = 406 (184.6 bits), Expect = 2.5e-60, Sum P(2) = 2.5e-60
Identities = 79/99 (79%), Positives = 83/99 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPQGQLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT TSY MHVVK PGQGLEWIG I P G T Y

Sbjct: 20 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYRMHVVKQRPQGQLEWIGIYINPSTGYTEY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARG 99
 NQKFK KA+LTAD SSSTAYMQ+SSLT EDSAVY+CARG
 Sbjct: 80 NQKFKDKATLTADKSSSTAYMQLSSLTFEDSAVYYCARG 118

Score = 71 (32.3 bits), Expect = 2.5e-60, Sum P(2) = 2.5e-60
 Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
 G DYWGQGT++TVSS
 Sbjct: 120 GVFDYWGQGTTLTVSS 135

>gp|Z22129|MDIGMVC_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 121

Score = 400 (181.8 bits), Expect = 2.8e-60, Sum P(2) = 2.8e-60
 Identities = 77/104 (74%), Positives = 87/104 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I P N T Y
 Sbjct: 1 EVLQQSGPELVKPGASVKMSCKASGYTFTSYVMHVVKQKPGQGLEWIGYINPYNDGTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEA 104
 N+KFKGKA+LT+D SSSTAYM++SSLTSSEDSAVY+CAR + G+
 Sbjct: 61 NEKFKGKATLTSKSSSTAYMELSSLTSSEDSAVYYCARRGYYS 104

Score = 77 (35.0 bits), Expect = 2.8e-60, Sum P(2) = 2.8e-60
 Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
 A+DYWGQGTSTVTVSS
 Sbjct: 107 AMDYWGQGTSTVTVSS 121

>pir|S26309|S26309 Ig heavy chain V region - mouse
 Length = 116

Score = 394 (179.1 bits), Expect = 2.9e-60, Sum P(2) = 2.9e-60
 Identities = 74/99 (74%), Positives = 84/99 (84%)

Query: 5 QQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYYNQKF 64
 QQSG+ELVR GASVK+SCKASGYT TSY MHVVKQ GQGLEWIGNI+PG+G T Y++KF
 Sbjct: 1 QQSGSELVRPGASVKLSCKASGYTFTSYMHVVKQQRHGQGLEWIGNIYPGSGSTNYDEKF 60

Query: 65 KGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWE 103
 K K +LT DTSSSTAYM +SSLTSSEDSAVY+C R +G
 Sbjct: 61 KSKGTLTVDTSSTAYMHLSSLTSSEDSAVYYCTREDDG 99

Score = 83 (37.7 bits), Expect = 2.9e-60, Sum P(2) = 2.9e-60
 Identities = 15/16 (93%), Positives = 16/16 (100%)

Query: 103 GALDYWGQGTSTVTVSS 118
 GA+DYWGQGTSTVTVSS
 Sbjct: 101 GAMDYWGQGTSTVTVSS 116

>gp|M32035|MUSIGHRI_1 Mouse Ig H-chain mRNA V-D-J region, from hybridoma
 P65D6-7, partial cds. [Mus musculus]
 Length = 121

Score = 411 (186.8 bits), Expect = 3.8e-60, Sum P(2) = 3.8e-60
 Identities = 78/103 (75%), Positives = 88/103 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++VVKQ PGQGLEWIG I PGNG T Y
 Sbjct: 1 EVLQQSGAELVRAGSSVKMSCKASGYTFTSYGINVVKQRPQGLEWIGYINPGNGYTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWE 103

N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR ++ G
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYG 103

Score = 65 (29.5 bits), Expect = 3.8e-60, Sum P(2) = 3.8e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118

DYWGQGT++TVSS

Sbjct: 109 DYWGQGTTLTVSS 121

>gp|S74051|S74051_1 Ig VH gene product [Mus sp.]
 Length = 114

Score = 471 (214.1 bits), Expect = 4.0e-60, P = 4.0e-60
 Identities = 86/114 (75%), Positives = 99/114 (86%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVK+SCKASGYT T Y MHWV+Q PGQGLEWIG I+PG+G+T Y

Sbjct: 1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYMMHWVRQRPQGQGLEWIGEIPGSGNTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSV 114

N+KF+GKA+LTAD SSSTAYMQ+SSLTSEDSAVYFCARG + +DYWGQGTSV

Sbjct: 61 NEKFRGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARGTLDYTM DYWGQGTSV 114

>pir|PH1482|PH1482 Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse
 (fragment)
 Length = 140

Score = 410 (186.4 bits), Expect = 4.5e-60, Sum P(2) = 4.5e-60
 Identities = 79/108 (73%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y

Sbjct: 20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGQGLEWIGYINPGNGYTKY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108

N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+

Sbjct: 80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYGGSYFF 127

Score = 65 (29.5 bits), Expect = 4.5e-60, Sum P(2) = 4.5e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118

DYWGQGT++TVSS

Sbjct: 128 DYWGQGTTLTVSS 140

>gp|x06110|MMIGVHD1_1 Mouse mRNA (36-35) for immunoglobulin heavy chain
 VDJ-region. [Mus musculus] >gp|M20274|MUSIGHKA_1 Mouse Ig active
 gamma chain mRNA V-region VDJH2, partial cds, clone 36-65. [Mus
 musculus] >gp|M20275|MUSIGHKB_1 Mouse Ig active gamma chain mRNA
 V-region VDJH2, partial cds, clone 4F8. [Mus musculus]
 >gp|M20276|MUSIGHKC_1 Mouse Ig active gamma chain mRNA V-region
 VDJH2, partial cds, clone 26C2. [Mus musculus]
 >gp|M20277|MUSIGHKD_1 Mouse Ig active gamma chain mRNA V-region
 VDJH2, partial cds, clone 24F3. [Mus musculus]
 >gp|M19292|MUSIGHXK_1 Mouse IgG active H-chain gene VDJ2-region
 from hybridoma cell-line 36-65. [Mus musculus]
 Length = 121

Score = 410 (186.4 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 79/108 (73%), Positives = 89/108 (82%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGQGLEWIGNIFPGNGDTYY 60

+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG T Y

Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPQGQGLEWIGYINPGNGYTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+
 Sbjct: 61 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYGGSYF 108

Score = 65 (29.5 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
 DYWGQGT++TVSS
 Sbjct: 109 DYWGQGTTLTVSS 121

>gp|Z22134|MDIGMVB1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 121

Score = 401 (182.3 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 77/99 (77%), Positives = 85/99 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
 + LQQSG ELV+ GASVKMSCKASGYT TSY MHVWKQ PGQGLEWIG I P N T Y
 Sbjct: 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTSYVMHVKQKPGQGLEWIGYINPYNDGTY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG 99
 N+KFKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CARG
 Sbjct: 61 NEKFKGKATLTSKSSSTAYMELSSLTSEDSAVYFCARG 99

Score = 74 (33.6 bits), Expect = 5.2e-60, Sum P(2) = 5.2e-60
 Identities = 13/15 (86%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTSS 118
 A+DYWG+GTSVTSS
 Sbjct: 107 AMDYWEGGTSTVTSS 121

>gp|K00684|MUSIGHBG1 Mouse Ig active H-chain V-region from B1-8.V1, subgroup
 VH-II. [Mus musculus]
 Length = 139

Score = 409 (185.9 bits), Expect = 6.2e-60, Sum P(2) = 6.2e-60
 Identities = 80/117 (68%), Positives = 92/117 (78%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYY 60
 Q LQQ GAELV+ GASVK+SCKASGYT TSY MHVWKQ PGQGLEWIG I P + DT Y
 Sbjct: 20 QVQLQPGAEVLKPGASVKVSKASGYTFTSYMHVWKQRPQGLEWIGRIHPSDSDTNY 79

Query: 61 NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
 NQKFKGKA+LT D SSTAYMQ+SSLTSEDSAVY+CAR ++ G+ + G T++
 Sbjct: 80 NQKFKGKATLTDKPSSTAYMQLSSLTSEDSAVYFCARYDYGGSYFDYWGQGTTLT 136

Score = 65 (29.5 bits), Expect = 6.2e-60, Sum P(2) = 6.2e-60
 Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTSS 118
 DYWGQGT++TVSS
 Sbjct: 127 DYWGQGTTLTVSS 139

>sp|P01747|HV03_MOUSE IG HEAVY CHAIN V REGION (36-65).
 Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
 Identities = 79/105 (75%), Positives = 88/105 (83%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHVWKQTPGQGLEWIGNIFPGNGDTYYNQK 63
 LQQSGAELVR+G+SVKMSCKASGYT TSY ++VWKQ PGQGLEWIG I PGNG T YN+K
 Sbjct: 3 LQQSGAELVRAGSSVKMSCKASGYTFTSYGINVWKQRPQGLEWIGYINPGNGYTYNEK 62

Query: 64 FKFKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEALDYW 108
 FKFK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G Y+

Sbjct: 63 FKGKTTTLVDKSSSTAYMQLRSLTSEDSAVYFCARSVYGGSYFF 107

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>pir|B22769|B22769 Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative
sequence)
Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 80/117 (68%), Positives = 92/117 (78%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQ GAELV+ GASVK+SCKASGYT TSY MHVVKQ PGQGLEWIG I P + DT Y
Sbjct: 1 QVQLQQPGAELVKPGASVKVSCASGYTFTSYMHVVKQRPQGLEWIGRIHPSDSDTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
NQKFKGKA+LT D SSTAYMQ+SSLTSEDSAVY+CAR ++ G+ + G T++
Sbjct: 61 NQKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVYFCARYDYGGSSYFDYWGQGTTLT 117

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>gp|M36216|MUSIGHADW_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 120

Score = 409 (185.9 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 80/117 (68%), Positives = 93/117 (79%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVVK PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKQRPQGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTS 117
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSAVYFCAR + + + G T++
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAVYFCARSYGGSSYFDYWGQGTTLT 117

Score = 65 (29.5 bits), Expect = 7.2e-60, Sum P(2) = 7.2e-60
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
DYWGQGT++TVSS

Sbjct: 108 DYWGQGTTLTVSS 120

>gp|L25855|MUSIGGB_1 IgG gene product [Mus musculus]
Length = 119

Score = 407 (185.0 bits), Expect = 7.3e-60, Sum P(2) = 7.3e-60
Identities = 76/98 (77%), Positives = 85/98 (86%)

Query: 4 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYYNQK 63
LQQSGAELV+ GASVK+SCK SGYT T Y + W+KQ P QGL WIG IFPG G TYYN+K
Sbjct: 4 LQQSGAELVKPGASVKLSCKTSGYTFTRYWIKQRPQGLEWIGEIFPGTGTTYNEK 63

Query: 64 FKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNW 101
FKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG++
Sbjct: 64 FKGKATLTIDTSSSTAYMQLSSLTSEDSAVYFCARGDY 101

Score = 67 (30.5 bits), Expect = 7.3e-60, Sum P(2) = 7.3e-60
Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
G DYWGQGT++TVSS
Sbjct: 104 GQEDYWGQGTTLTVSS 119

>gp|S77022|S77022_1 anti-CD29 antibody heavy chain variable region [Mus sp.]
Length = 116

Score = 403 (183.2 bits), Expect = 7.5e-60, Sum P(2) = 7.5e-60
Identities = 74/97 (76%), Positives = 86/97 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQ+SG ELVR GASVK+SCKASGYT T Y + WVKQ PGQGLEWI I+PG+G+T+Y
Sbjct: 1 QVQLQESGTELVRPGASVKLSCKASGYTFTDYYISWVKQRPQGLEWIARIYPGSGNTFY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSSEDSAVYFCA 97
N+KFKGKA+LTA+TSS+TAYMQ+SSLTSEDSAVYFCA
Sbjct: 61 NEKFKGKATLTAETSSNTAYMQLSSLTSEDSAVYFCA 97

Score = 71 (32.3 bits), Expect = 7.5e-60, Sum P(2) = 7.5e-60
Identities = 13/16 (81%), Positives = 15/16 (93%)

Query: 103 GALDYWGQGTSTVTVSS 118
G+ DYWGQGT+VTVSS
Sbjct: 101 GSGDYWGQGTTVTVSS 116

>gp|M36225|MUSIGHAEF_1 immunoglobulin heavy chain V-region [Mus musculus]
Length = 118

Score = 468 (212.8 bits), Expect = 9.9e-60, P = 9.9e-60
Identities = 92/118 (77%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSGAEL + GASVKMSCKASGYT TSY MHWVKQ PGQGLEWIG I P G T Y
Sbjct: 1 QVQLQQSGAELAKPGASVKMSCKASGYTFTSYNMHWVKQRPQGLEWIGYINPSTGYTEY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVTVSS 118
NQKFK KA+LTAD SSSTAYMQ+SSLTSEDSA+Y+CAR + A+DYWGQGTSTVTVSS
Sbjct: 61 NQKFKDKATLTADKSSSTAYMQLSSLTSEDSALYYCARWVYYYAMDYWGQGTSTVTVSS 118

>pir|S40295|S40295 Ig gamma-2a chain (mAb735) - mouse
Length = 446

Score = 420 (190.9 bits), Expect = 1.1e-59, Sum P(2) = 1.1e-59
Identities = 79/99 (79%), Positives = 88/99 (88%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY 60
Q LQQSG ELVR GASVK+SCKASGYT T Y +HWVKQ PG+GLEWIG I+PG+G+T Y
Sbjct: 1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLWIGWIYPGSGNTKY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSSEDSAVYFCARG 99
N+KFKGKA+LT DTSSSTAYMQ+SSLTSEDSAVYFCARG
Sbjct: 61 NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 77 (35.0 bits), Expect = 1.1e-59, Sum P(2) = 1.1e-59
Identities = 14/15 (93%), Positives = 15/15 (100%)

Query: 104 ALDYWGQGTSTVTVSS 118
A+DYWGQGTSTVTVSS
Sbjct: 103 AMDYWGQGTSTVTVSS 117

>gp|L22749|MUSI_1 immunoglobulin heavy chain [Mus musculus]
Length = 118

Score = 467 (212.3 bits), Expect = 1.4e-59, P = 1.4e-59
Identities = 89/118 (75%), Positives = 101/118 (85%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQSGAELVR G SVKMSCKA+GYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
Sbjct: 1 QVQLQQSGAELVRPGTSVKMSCKAAGYTFITNYWIGWVKRPGHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVSS 118
N+KFKGKA+LTADTSSSTAYMQ+SSLTSEDSA+Y+CAR + A+DYWGQGTSTVSS
Sbjct: 61 NEKFKGKATLTADTSSSTAYMQLSSLTSEDSAIYYCARPFYFAMDYWGQGTSTVSS 118

>gp|M61026|MUSIGHAANN_1 immunoglobulin heavy chain VDJ region [Mus musculus]
Length = 118

Score = 467 (212.3 bits), Expect = 1.4e-59, P = 1.4e-59
Identities = 89/118 (75%), Positives = 99/118 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
Q LQQ GAELV+ GASVK+SCKASGYT TSY MHVVKQ PG+GLEWIG I P +G T Y
Sbjct: 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYLMHVVKRPGRGLEWIGRIDPNSGGTKY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTVSS 118
N+KFK KA+LT D SSTAYMQ+SSLTSEDSAVY+CAR + GA+DYWGQGTSTVSS
Sbjct: 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYYYGGAMDYWGQGTSTVSS 118

>gp|M31287|MUSIGHAVA_1 IgG gene product [Mus musculus]
Length = 115

Score = 466 (211.8 bits), Expect = 1.9e-59, P = 1.9e-59
Identities = 88/115 (76%), Positives = 96/115 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
+ LQQSG L R GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I+PGN DT Y
Sbjct: 1 EVQLQQSGTVLARPASVKMSCKASGYTFTSYMHVVKRPGQGLEWIGAIYPGNSDTRY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTV 115
NQKFKGKA LTA TS+STAYM++SSLT+EDSAVY+C RG A+DYWGQGTSTV
Sbjct: 61 NQKFKGKAKLTAVTSASTAYMELSSLTNEEDSAVYYCTRGGLFTAMDYWGQGTSTV 115

>gp|M31288|MUSIGHAWA_1 Mouse active rheumatoid factor IgA chain (family J558)
mRNA J4 region, partial cds, hybridoma AM15. [Mus musculus]
Length = 115

Score = 466 (211.8 bits), Expect = 1.9e-59, P = 1.9e-59
Identities = 88/115 (76%), Positives = 96/115 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
+ LQQSG L R GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I+PGN DT Y
Sbjct: 1 EVQLQQSGTVLARPASVKMSCKASGYTFTSYMHVVKRPGQGLEWIGAIYPGNSDTSY 60

Query: 61 NQKFKGKASLTADTSSSTAYMQISLTSSEDSAVYFCARGNWEALDYWGQGTSTV 115
NQKFKGKA LTA TS+STAYM++SSLT+EDSAVY+C RG A+DYWGQGTSTV
Sbjct: 61 NQKFKGKAKLTAVTSASTAYMELSSLTNEEDSAVYYCTRGGLFTAMDYWGQGTSTV 115

>gp|M31908|MUSIGHRC_1 Mouse Ig H-chain V-D-J region mRNA, from hybridoma
hVH65-211, partial cds. [Mus musculus]
Length = 121

Score = 404 (183.7 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
Identities = 77/103 (74%), Positives = 86/103 (83%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHVVKQTPGGGLEWIGNIFPGNGDTYY 60
+ LQQSGAELVR+G+SVKMSCKASGYT TSY ++WVKQ PGQGLEWIG I PGNG Y
Sbjct: 1 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKRPGQGLEWIGYINPGNGYIKY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCARGNWEG 103
 N+KFKGK +LT D SSSTAYMQ+ SLTSEDSAVYFCAR + G
 Sbjct: 61 NEKFKGKATLTVDKSSSTAYMQLRSLTSEDSAVYFCARSEYYG 103

Score = 66 (30.0 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 11/15 (73%), Positives = 14/15 (93%)

Query: 104 ALDYWGQGTSTVTVSS 118
 + DYWGQGT++TVSS
 Sbjct: 107 SFDYWGGGTTTLTVSS 121

>gp|M36226|MUSIGHAEG_1 immunoglobulin heavy chain V-region [Mus musculus]
 Length = 120

Score = 414 (188.2 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 79/99 (79%), Positives = 87/99 (87%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGGGLEWIGNIFPGNGDTYY 60
 Q LQQSGAELVR G SVK+SCKASGYT T+Y + WVKQ PG GLEWIG+I+PG G T Y
 Sbjct: 1 QVQLQQSGAELVRPGTSVKISCKASGYTFTNYWLGWVKQRPBGHGLEWIGDIYPGGGYTNY 60

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCARG 99
 N+KFKGKA+LTADTSSTAYMQ+SSLTSEDSAVYFCARG
 Sbjct: 61 NEKFKGKATLTADTSSTAYMQLSSLTSEDSAVYFCARG 99

Score = 56 (25.5 bits), Expect = 2.5e-59, Sum P(2) = 2.5e-59
 Identities = 10/12 (83%), Positives = 11/12 (91%)

Query: 107 YWGQGTSTVTVSS 118
 YWGQGT VTVS+
 Sbjct: 109 YWGQGTTLTVSA 120

>gp|U36491|MMU36491_1 J558+ IgM heavy chain [Mus musculus]
 Length = 109

Score = 402 (182.7 bits), Expect = 2.8e-59, Sum P(2) = 2.8e-59
 Identities = 75/95 (78%), Positives = 81/95 (85%)

Query: 7 SGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGGGLEWIGNIFPGNGDTYYNQKFKG 66
 SG ELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIGNI P NG T YN+KFK
 Sbjct: 1 SGTSLVKGASVKLSCKASGYTFTSYNMHWKQRPGGGLEWIGNINPNSGGTNYNEKFKS 60

Query: 67 KASLTADTSSTAYMQISLTSEDSAVYFCARGNW 101
 KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR W
 Sbjct: 61 KATLTVDKSSSTAYMQLSSLTSEDSAVYFCARSGW 95

Score = 68 (30.9 bits), Expect = 2.8e-59, Sum P(2) = 2.8e-59
 Identities = 12/16 (75%), Positives = 14/16 (87%)

Query: 103 GALDYWGQGTSTVTVSS 118
 G DYWGQGT++TVSS
 Sbjct: 94 GWFYWGQGTTLTVSS 109

>gp|L35315|MUSIVDJA_1 immunoglobulin heavy chain [Mus musculus]
 Length = 143

Score = 404 (183.7 bits), Expect = 2.9e-59, Sum P(2) = 2.9e-59
 Identities = 77/98 (78%), Positives = 83/98 (84%)

Query: 1 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWKQTPGGGLEWIGNIFPGNGDTYY 60
 Q LQQ G ELV+ GASVK+SCKASGYT TSY MHWVKQ PGQGLEWIGNI P NG T Y
 Sbjct: 20 QVQLQQPGTELKPGASVKLSCKASGYTFTSYNMHWKQRPGGGLEWIGNINPNSGGTNY 79

Query: 61 NQKFKGKASLTADTSSTAYMQISLTSEDSAVYFCAR 98
 N+KFK KA+LT D SSSTAYMQ+SSLTSEDSAVY+CAR

Sbjct: 80 NEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR 117

Score = 65 (29.5 bits), Expect = 2.9e-59, Sum P(2) = 2.9e-59
Identities = 11/13 (84%), Positives = 13/13 (100%)

Query: 106 DYWGQGTSTVTVSS 118
DYWGQGT++TVSS

Sbjct: 128 DYWGQGTTLTVSS 140

>gp|X88902|MMVARHECH_1 Fv fragment variable heavy chain [Mus musculus]
Length = 131

Score = 389 (176.8 bits), Expect = 3.2e-59, Sum P(2) = 3.2e-59
Identities = 75/95 (78%), Positives = 83/95 (87%)

Query: 4 LQSGAELVRSGASVKMSCKASGYTLTSYMHVVKQTPGQGLEWIGNIFPGNGDTYYNQK 63
LQ+SGA LV+ GASVKMSCKASGYT TSY MHVVKQ PGQGLEWIG I P N T YN+K

Sbjct: 4 LQESGAGLVKPGASVKMSCKASGYTFTSYMHVVKQKPGQGLEWIGYINPYNDGTYNEK 63

Query: 64 FKGKASLTADTSSSTAYMQISLTSEDSAVYFCAR 98
FKGKA+LT+D SSSTAYM++SSLTSEDSAVY+CAR

Sbjct: 64 FKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCAR 98

Score = 80 (36.4 bits), Expect = 3.2e-59, Sum P(2) = 3.2e-59
Identities = 14/18 (77%), Positives = 16/18 (88%)

Query: 101 WEGALDYWGQGTSTVTVSS 118
W A+DYWGQGT+VTVSS

Sbjct: 105 WYYAMDYWGQGTTVTVSS 122

WARNING: HSPs involving 8585 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100

B=50

H=1

-qtype

E=10

-ctxfactor=1.00

Query	Frame	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+0	0	BLOSUM62	0.315	0.127	0.386	same	same	same	

Query	Frame	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+0	0		118	118	10.	59	3	11	22	0.18	31

Statistics:

Query	Frame	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+0	0		63 (28.6 bits)	542 (246.4 bits)	17989	94

Query	Frame	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+0	0		3523	12605070	3175944	9368862	60214	834

Database: Non-redundant PDB+SwissProt+SPupdate+PIR+GenPept+GPupdate

Release date: 5:56 AM EST Jan 19, 1996

Posted date: 5:57 AM EST Jan 19, 1996

of letters in database: 51,001,589

of sequences in database: 172,206

of database sequences satisfying E: 8635

No. of states in DFA: 546 (54 KB)

Total size of DFA: 92 KB (128 KB)

11D10 Heavy Chain PEPTIDE – 21

Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 8
Time to search database: 82.38u 1.48s 83.86t Real: 00:00:17
Total cpu time: 82.47u 1.53s 84.00t Real: 00:00:18

WARNINGS ISSUED: 2

S. Chatterjee

===== 1121

Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>

Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTP id 5094; Fri, 19 Jan 1996 16:19:56 -0500

Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP; Fri, 19 Jan 96 16:19:54 EST

Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov id QAA16046; Fri, 19 Jan 1996 16:19:43 -0500

Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6) id QAA21085; Fri, 19 Jan 1996 16:19:43 -0500

Date: Fri, 19 Jan 1996 16:19:43 -0500

Message-Id: <199601192119.QAA21085@blaster.nlm.nih.gov>

To: SKCHAT00@UKCC.uky.edu

Subject: Results-BLAST Server

From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>

Errors-To: <owner-blast@ncbi.nlm.nih.gov>

Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>

==+=====

To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov' with the word HELP in the body of the message. The documentation was last modified March 18th.

==+=====

March 18, 1995

The BLAST FAQ was updated with the question Q33 related to degenerated nucleotide code available for the BLAST programs.

==+=====

August 8, 1995

A new server directive ACKNOWLEDGE, has been added to the server. See the help file for more details.

==+=====

Trying blaster... connected

National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 16:16:50 EST 1996, Up 30 days, 4:08, 0 user, load: 14.58, 13.81, 14.79

PEPTIDE SEQUENCE DATABASES

nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GPUUpdate, updated daily for efficient, complete searches of the five component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release

swissprot SWISS-PROT Release 32.0, December 1995

pir PIR Release 45.0 (complete), June 30, 1995

spupdate SWISS-PROT cumulative weekly update to the major release

genpept CDS translations from GenBank(R) Release 92, December 15, 1995

gpupdate cumulative daily updates to the major release of genpept

kabatpro Kabat Sequences of Proteins of Immunological Interest, June 1995

tfd TFD transcription factor (protein) database Release 7.0, June 1993

alu * Translations of select Alu repeats from REPBASE

NUCLEOTIDE SEQUENCE DATABASES

nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily for efficient, complete searches of the four component databases:

pdb Brookhaven Protein Data Bank, April 1995 Release

genbank GenBank(R) Release 92 (no daily updates), December 15, 1995

gbupdate GenBank(R) cumulative daily updates to the major release

embl EMBL Data Library, Release 45.0, December 1995

emblu EMBL Data Library cumulative daily updates to the major release

vector Vector subset of GenBank(R), February 3rd, 1995

alu ** Select Alu repeats from REPBASE

kabatsnuc Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995

epd Eukaryotic Promoter Database Release 43, June 1995

dbest + Database of Expressed Sequence Tags (cumulative daily update)

dbsts + Database of Sequence Tagged Sites Release 1.5, October 26, 1994

[illegible]

72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081

[illegible][illegible][illegible]

0.016	3864	27	:
0.010	3837	22	:
0.0063	3815	19	:
0.0040	3796	28	:
0.0025	3768	20	:
0.0016	3748	13	:

			High	Smallest	
Sequences producing High-scoring Segment Pairs:			Score	Sum Probability P(N)	N
gp L41880	MUSIKCC_1	immunoglobulin kappa chain [Mus mu...	491	4.7e-63	1
gp J00550	MUSIGKAC2_1	immunoglobulin kappa chain variabl...	486	2.1e-62	1
sp P01639	KV5G_MOUSE	IG KAPPA CHAIN PRECURSOR V-V REGIO...	486	2.3e-62	1
gp V00808	MMIGK7_1	immunoglobulin kappa [Mus musculus]	481	1.1e-61	1
pir PL0260	PL0260	Ig kappa chain V region (anti-DNA,...	481	1.4e-61	1
gp M59920	MUSIGKAA3_1	Ig kappa chain [Mus musculus]	480	1.9e-61	1
pir PL0259	PL0259	Ig kappa chain V region (anti-DNA,...	477	4.8e-61	1
gp Z22118	MDIGKVBS_1	immunoglobulin variable region [Mu...	461	7.5e-59	1
gp M36246	MUSIGLAFA_1	immunoglobulin kappa-chain VK-1 [M...	455	5.3e-58	1
pdb 2GFB	A	Igg2a Fab Fragment (Cnj206) >pdb 2...	447	3.1e-57	1
gp M64168	MUSIGKAF1_1	immunoglobulin kappa-chain VK-1 [M...	446	9.0e-57	1
pir PL0262	PL0262	Ig kappa chain V region (anti-DNA,...	439	7.9e-56	1
gp X02177	MMIGGVJ1_1	Immunoglobulin G kappa light chain...	431	8.3e-55	1
gp U25098	MMU25098_1	immunoglobulin light chain [Mus mu...	430	1.3e-54	1
gp V00804	MMIGK3_1	kappa-immunoglobulin [Mus musculus...	427	3.2e-54	1
gp U29617	MMU29617_1	Ig kappa chain [Mus musculus]	427	3.9e-54	1
gp X02178	MMIGGVJ2_1	immunoglobulin G kappa light chain...	426	4.0e-54	1
pir B47271	B47271	nitrophenyl phosphonate-specific a...	425	6.4e-54	1
gp M12191	MUSIGKCMA_1	Mouse Ig active kappa-chain VJ2C m...	419	3.6e-53	1
pir PH1062	PH1062	Ig light chain V region (clone 202...	415	1.7e-52	1
gp S69053	S69053_1	anti-p-nitrophenyl phosphonate est...	415	1.7e-52	1
pir PL0261	PL0261	Ig kappa chain V region (anti-DNA,...	399	2.9e-50	1
gp U30236	MMU30236_1	Ig kappa chain [Mus musculus]	396	6.7e-50	1
gp U19320	MMU19320_1	immunoglobulin kappa light chain v...	396	6.8e-50	1
pir C28840	C28840	Ig kappa chain V region (HP22) - m...	387	1.1e-48	1
pir B28840	B28840	Ig kappa chain V region (HP27) - m...	387	1.1e-48	1
gp X03382	MMIGKGA1_1	Mouse mRNA for GAT (HP27) anti-idi...	387	1.1e-48	1
gp X03383	MMIGKGA2_1	Mouse mRNA for GAT (HP22) anti-idi...	386	1.6e-48	1
pir D32513	D32513	Ig kappa chain precursor V region ...	385	1.6e-48	1
gp U20061	MMU20061_1	immunoglobulin kappa chain [Mus mu...	381	7.0e-48	1
gp M33559	MUSIGKABE_1	Mouse Ig rearranged kappa-chain mR...	381	7.0e-48	1
pir PL0220	PL0220	Ig kappa chain V region (G) - mous...	371	1.7e-46	1
pir D28840	D28840	Ig kappa chain V region (HP29) - m...	371	1.9e-46	1
gp J00568	MUSIGKAE_1	mouse ig kappa unproductively rear...	369	2.6e-46	1
gp S76654	S76654_1	F30C7 light chain variable region ...	368	4.3e-46	1
gp M36261	MUSIGLAFF_1	immunoglobulin kappa-chain VK-1 [M...	367	5.8e-46	1
gp X55042	MMIGKL221_1	immunoglobulin kappa light chain [...	300	6.6e-46	2
sp P01641	KV5H_MOUSE	IG KAPPA CHAIN PRECURSOR V-V REGIO...	365	1.0e-45	1
pir JL0080	JL0080	Ig light chain precursor V region ...	365	1.0e-45	1
pir A38740	A38740	Ig kappa chain V region (Py20) - m...	365	1.1e-45	1
sp P01643	KV5J_MOUSE	IG KAPPA CHAIN V-V REGION (MOPC 17...	365	1.1e-45	1
gp X55044	MMIGKL229_1	immunoglobulin kappa light chain [...	365	1.1e-45	1
gp U21066	MMU21066_1	immunoglobulin kappa chain variabl...	365	1.3e-45	1
gp U16180	MMU16180_1	Ig light chain [Mus musculus]	364	1.5e-45	1
gp Z37332	HSIGVKC45_1	immunoglobulin kappa light chain v...	300	1.6e-45	2
gp M36236	MUSIGLAEQ_1	immunoglobulin kappa-chain VK-1 [M...	363	2.1e-45	1
gp X55047	MMIGKL4A1_1	immunoglobulin kappa light chain [...	300	2.3e-45	2
pir S38862	S38862	Ig kappa chain V region - mouse >g...	299	4.3e-45	2
gp L35316	MUSIVJR_1	immunoglobulin light chain [Mus mu...	360	4.4e-45	1
gp U16689	MMU16689_1	immunoglobulin light chain precurs...	360	4.5e-45	1
pdb 2F19	L	Fab Fragment From A Monoclonal Ant...	358	5.0e-45	1
pdb 6FAB	L	Antigen-Binding Fragment Of The Mu...	358	5.0e-45	1
pir E38740	E38740	Ig kappa chain V region (Py54) - m...	360	5.1e-45	1
gp X55041	MMIGKL218_1	immunoglobulin kappa light chain [...	360	5.3e-45	1
gp M14840	MUSIGKBP_1	Mouse IgM monoclonal anti-BrMRBC a...	360	5.3e-45	1
sp P01644	KV5K_MOUSE	IG KAPPA CHAIN V-V REGION (HP R16...	359	7.2e-45	1

gp M34593 MUSIGKABW_1	Mouse Ig kappa-chain mRNA V-J regi...	359	7.2e-45	1
gp M15519 MUSIGKCM_1	Mouse allele 91A3 V-region kappa c...	358	8.4e-45	1
pdb 1F81 L	Fab Fragment Of The Monoclonal Ant...	356	9.4e-45	1
pir G38740 G38740	Ig kappa chain V region (Py69) - m...	358	9.7e-45	1
sp P01648 KV50_MOUSE	IG KAPPA CHAIN V-V REGION (HP 91A3).	358	9.9e-45	1
gp S77030 S77030_1	H4-specific antibody light chain v...	358	9.9e-45	1
pir PH1224 PH1224	Ig kappa chain precursor V region ...	357	1.2e-44	1
gp X53329 MMHS2H1VL_1	2H1 VL gene product [Mus musculus]	357	1.2e-44	1
sp P01646 KV5N_MOUSE	IG KAPPA CHAIN V-V REGION (HP 123E6).	357	1.4e-44	1
sp P01647 KV5N_MOUSE	IG KAPPA CHAIN V-V REGION (HP 124E1).	357	1.4e-44	1
pir C26405 C26405	Ig kappa chain V region (3D10) - m...	357	1.4e-44	1
pir S19970 S19970	Ig kappa chain V region (M-T151) - ...	357	1.4e-44	1
gp M32043 MUSIGKCR_1	Mouse Ig kappa-chain mRNA V-J regi...	357	1.4e-44	1
pir S32188 S32188	Ig kappa chain V region - mouse (f...	357	1.4e-44	1
gp L01279 HUMIGKVCA_1	immunoglobulin kappa chain [Homo s...	297	1.5e-44	2
gp U05217 MMU05217_1	anti-platelet integrin gpIIb/IIIa ...	356	1.6e-44	1
gp X06111 MMIGKVJ2_1	Mouse (hVH65-107) mRNA for immunog...	356	1.9e-44	1
gp X05796 MMIGVK36_1	immunoglobulin L chain [Mus muscul...	356	1.9e-44	1
gp M31915 MUSIGKCRO_1	Mouse Ig light-chain V-J region mR...	356	1.9e-44	1
pir B28044 B28044	Ig kappa chain V region (GP1) - mouse	356	1.9e-44	1
gp M37021 MUSIGKADT_1	Mouse Ig rearranged kappa-chain mR...	356	1.9e-44	1
gp M36242 MUSIGKAEW_1	immunoglobulin kappa-chain VK-1 [M...	356	1.9e-44	1
gp M15402 RATIGKAC_1	Rat Ig active kappa-chain mRNA VJ-...	355	2.0e-44	1
pir B23986 B23986	Ig kappa chain precursor V region ...	355	2.1e-44	1
pir A34904 A34904	Ig kappa chain precursor V region ...	355	2.2e-44	1
pir A29380 A29380	Ig kappa chain precursor V region ...	355	2.3e-44	1
pir C38740 C38740	Ig kappa chain V region (Py2) - mouse	355	2.5e-44	1
pir PL0282 PL0282	Ig light chain V region (45-49, an...	355	2.6e-44	1
gp M34590 MUSIGKABT_1	Mouse Ig kappa-chain mRNA V-J regi...	355	2.6e-44	1
gp M32040 MUSIGKCRQ_1	Mouse Ig kappa-chain mRNA V-J regi...	355	2.6e-44	1
gp S74560 S74560_1	rheumatoid factor RF3-2C [Mus sp.]	355	2.6e-44	1
gp M59918 MUSIGKAA1_1	Ig kappa chain [Mus musculus] >gp ...	354	2.9e-44	1
pir A26406 A26406	Ig kappa chain V region (Ars-A) - ...	354	3.0e-44	1
sp P01645 KV5L_MOUSE	IG KAPPA CHAIN V-V REGION (HP 93G7).	354	3.5e-44	1
pir B26405 B26405	Ig kappa chain V region (1F6) - mouse	354	3.5e-44	1
pir B30551 B30551	Ig kappa chain V region (36-71) - ...	354	3.5e-44	1
gp M33678 MUSIGKABF_1	Mouse Ig rearranged L-chain mRNA V...	354	3.5e-44	1
gp M60020 MUSIGKAAAM_1	Ig kappa chain [Mus musculus]	353	4.1e-44	1
gp X72463 HSIGKLV42_1	Ig kappa light chain (VJC) [Homo s...	353	4.1e-44	1
pir S40353 S40353	Ig kappa light chain (VJC) - human.	353	4.2e-44	1
gp L39092 MUSIGK527A_1	anti-fluorescein antibody [Mus mus...	352	5.7e-44	1
pir B48677 B48677	Ig light chain V-J region (44.1) - ...	352	6.7e-44	1
gp M36256 MUSIGLAFK_1	immunoglobulin kappa-chain VK-1 [M...	352	6.7e-44	1
gp S77025 S77025_1	H2A/H2B-specific antibody light ch...	352	6.7e-44	1

WARNING: Descriptions of 5103 database sequences were not reported due to the limiting value of parameter V = 100.

>gp|L41880|MUSIKCC_1 immunoglobulin kappa chain [Mus musculus]
Length = 130

Score = 491 (223.7 bits), Expect = 4.7e-63, P = 4.7e-63
Identities = 99/107 (92%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLSGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFGSGRSRSGSDYSLTISSLESDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGRSRSGSDYSLTISSLES DFV YYCLQYASSPYTFGGGKLEIK
Sbjct: 83 RFGSGRSRSGSDYSLTISSLESEDFVYYCLQYASSPYTFGGGKLEIK 129

>gp|J00550|MUSIGKAC2_1 immunoglobulin kappa chain variable region [Mus musculus]
Length = 146

Score = 486 (221.4 bits), Expect = 2.1e-62, P = 2.1e-62
Identities = 98/107 (91%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>sp|P01639|KV5G_MOUSE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
>pir|A93211|KVMSM4 Ig kappa chain precursor V region (MOPC 41) -
mouse
Length = 130

Score = 486 (221.4 bits), Expect = 2.3e-62, P = 2.3e-62
Identities = 98/107 (91%), Positives = 102/107 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>gp|V00808|MMIGK7_1 immunoglobulin kappa [Mus musculus]
Length = 130

Score = 481 (219.1 bits), Expect = 1.1e-61, P = 1.1e-61
Identities = 97/107 (90%), Positives = 101/107 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCR SQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRPSQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEIK
Sbjct: 83 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEIK 129

>pir|PL0260|PL0260 Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
Length = 106

Score = 481 (219.1 bits), Expect = 1.4e-61, P = 1.4e-61
Identities = 97/106 (91%), Positives = 101/106 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
RFSGSRSGSDYSLTISSLES DFV YYCLQYASSP+TFGGGKLEI
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGGGKLEI 106

>gp|M59920|MUSIGKAA3_1 Ig kappa chain [Mus musculus]
Length = 107

Score = 480 (218.7 bits), Expect = 1.9e-61, P = 1.9e-61
Identities = 97/106 (91%), Positives = 101/106 (95%)

Query: 2 IQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKR 61
IQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKR
Sbjct: 1 IQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKR 60

Query: 62 FSGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 FSGSRSGSDYSLTISLES DFV YYCLQYASSP+TFGGGKLEIK
 Sbjct: 61 FSGSRSGSDYSLTISSESEDFVDYYCLQYASSPWTFGGGKLEIK 106

>pir|PL0259|PL0259 Ig kappa chain V region (anti-DNA, DP11VK) - mouse
 (fragment)
 Length = 106

Score = 477 (217.3 bits), Expect = 4.8e-61, P = 4.8e-61
 Identities = 96/106 (90%), Positives = 101/106 (95%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGRSLNLWQQEPDGTIKRLIYATSSLD SGVPK 60

Query: 61 RFGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEI 106
 RFGSRSGSDYSLTISLES DFV YYCLQYA+SP+TFGGGKLEI
 Sbjct: 61 RFGSRSGSDYSLTISSESEDFVDYYCLQYATSPWTFGGGKLEI 106

>gp|222118|MDIGKVB5_1 immunoglobulin variable region [Mus musculus domesticus]
 Length = 107

Score = 461 (210.0 bits), Expect = 7.5e-59, P = 7.5e-59
 Identities = 93/107 (86%), Positives = 98/107 (91%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIY+TS+L SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYSTSTLNSGVPK 60

Query: 61 RFGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSLTISLES DF YYCLQYASSPYTFGGGKLEIK
 Sbjct: 61 RFGSRSGSDYSLTISSESEDFADYYCLQYASSPYTFGGGKLEIK 107

>gp|M36246|MUSIGLAFA_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
 Length = 101

Score = 455 (207.3 bits), Expect = 5.3e-58, P = 5.3e-58
 Identities = 92/101 (91%), Positives = 95/101 (94%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
 SPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSR
 Sbjct: 1 SPSSLSASLGERVSLTCRASQDIGSSNLWQQEPDGTIKRLIYATSSLD SGVPKRFSGSR 60

Query: 67 SGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 SGSDYSLTISLES DFV YYCLQYASSPYTFGGGKLEIK
 Sbjct: 61 SGSDYSLTISSESEDFVDYYCLQYASSPYTFGGGKLEIK 101

>pdb|2GFB|A Igg2a Fab Fragment (Cnj206) >pdb|2GFB|C Igg2a Fab Fragment (Cnj206)
 >pdb|2GFB|E Igg2a Fab Fragment (Cnj206) >pdb|2GFB|G Igg2a Fab
 Fragment (Cnj206) >pdb|2GFB|I Igg2a Fab Fragment (Cnj206)
 >pdb|2GFB|K Igg2a Fab Fragment (Cnj206) >pdb|2GFB|M Igg2a Fab
 Fragment (Cnj206) >pdb|2GFB|O Igg2a Fab Fragment (Cnj206)
 Length = 214

Score = 447 (203.6 bits), Expect = 3.1e-57, P = 3.1e-57
 Identities = 91/105 (86%), Positives = 95/105 (90%)

Query: 2 IQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKR 61
 IQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPKR
 Sbjct: 2 IQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASLD SGVPKR 61

Query: 62 FSGSRSGSDYSLTISLESQDFVAYYCLQYASSPYTFGGGKLEI 106
 FSGSRSGSDYSLTISLES DF YYCLQYASSPYTFGGGKLEI
 Sbjct: 62 FSGSRSGSDYSLTISSESEDFADYYCLQYASSPYTFGGGKLEI 106

>gp|M64168|MUSIGKFT_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
Length = 102

Score = 446 (203.2 bits), Expect = 9.0e-57, P = 9.0e-57
Identities = 90/101 (89%), Positives = 94/101 (93%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
SPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSR
Sbjct: 2 SPSSLSASLGERVSLTCRASQDIGNSLNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSR 61

Query: 67 SGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
SGSDYSLTISSLES DFV YYCLQYAS YTFGGGTKLE+K
Sbjct: 62 SGSDYSLTISSLESEDFVYYCLQYASYTTYTFGGGTKLELK 102

>pir|PL0262|PL0262 Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
Length = 106

Score = 439 (200.0 bits), Expect = 7.9e-56, P = 7.9e-56
Identities = 89/106 (83%), Positives = 94/106 (88%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+IG L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLACRASQEIIGGYLSWLQQKPDGTIKRLIYAASLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEI 106
RF GSRSGSDYSLTISSLES DF YYCLQYAS P+TFGGGTKLEI
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPTFGGGTKLEI 106

>gp|X02177|MMIGGVJ1_1 Immunoglobulin G kappa light chain [Mus musculus]
Length = 126

Score = 431 (196.4 bits), Expect = 8.3e-55, P = 8.3e-55
Identities = 88/107 (82%), Positives = 93/107 (86%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 14 DIQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPK 73

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
RFSGSRSGSDYSLTISSLES DF YYCLQY S P TFG GTKLE+K
Sbjct: 74 RFSGSRSGSDYSLTISSLESEDFADYYCLQYLSYPLTFGAGTKLELK 120

>gp|U25098|MMU25098_1 immunoglobulin light chain [Mus musculus]
Length = 112

Score = 430 (195.9 bits), Expect = 1.3e-54, P = 1.3e-54
Identities = 87/107 (81%), Positives = 94/107 (87%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
++QMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
Sbjct: 1 ELQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPK 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLEIK 107
RFSGSRSGSDYSLTISSLES DF YYCLQYAS P TFG GTKLE+K
Sbjct: 61 RFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPLTFGAGTKLELK 107

>gp|V00804|MMIGK3_1 kappa-immunoglobulin [Mus musculus] >gp|J00566|MUSIGKVC_1
Mouse ig kappa germline v gene: vk4.1. [Mus musculus]
Length = 117

Score = 427 (194.5 bits), Expect = 3.2e-54, P = 3.2e-54
Identities = 87/95 (91%), Positives = 90/95 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 82

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSP 95
 RFGSRSGSDYSLTISSLES DFV YYCLQYASSP
 Sbjct: 83 RFGSRSGSDYSLTISSLESEDFVDYYCLQYASSP 117

>gp|U29617|MMU29617_1 Ig kappa chain [Mus musculus]
 Length = 95

Score = 427 (194.5 bits), Expect = 3.9e-54, P = 3.9e-54
 Identities = 87/95 (91%), Positives = 90/95 (94%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPK
 Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPK 60

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSP 95
 RFGSRSGSDYSLTISSLES DFV YYCLQYASSP
 Sbjct: 61 RFGSRSGSDYSLTISSLESEDFVDYYCLQYASSP 95

>gp|X02178|MMIGGVJ2_1 immunoglobulin G kappa light chain [Mus musculus]
 Length = 127

Score = 426 (194.1 bits), Expect = 4.0e-54, P = 4.0e-54
 Identities = 87/107 (81%), Positives = 92/107 (85%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
 Sbjct: 15 DIQMTQSPSSLSASLGERVSLTCRASQEI SGYLSWLQQKPDGTIKRLIYAASLD SGVPK 74

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSLTISSLES DF YYCLQY S P TFG GTKLE+K
 Sbjct: 75 RFGSRSGSDYSLTISSLESEDFADYYCLQYLYPLTFGAGTKLELK 121

>pir|B47271|B47271 nitrophenyl phosphonate-specific antibody 48G7 light chain
 VJ - Escherichia coli (fragment) >gp|S55170|S55170_1 nitrophenyl
 phosphonate-specific antibody 48G7 light chain VJ [Mus sp.]
 Length = 108

Score = 425 (193.6 bits), Expect = 6.4e-54, P = 6.4e-54
 Identities = 87/107 (81%), Positives = 94/107 (87%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 ++ +TQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIYA S+L SGVPK
 Sbjct: 2 ELVLTQSPSSLSASLGERVSLTCRASQEI NGYLGWLQQKPDGTIKRLIYAASLDHSGVPK 61

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSLTISSLES DF YYCLQYAS P TFGGGKLEIK
 Sbjct: 62 RFGSRSGSDYSLTISSLESEDFADYYCLQYASYPRTFGGGKLEIK 108

>gp|M12191|MUSIGKMA_1 Mouse Ig active kappa-chain VJ2C mRNA from plasmacytoma
 MOPC 1738, partial cds. [Mus musculus]
 Length = 127

Score = 419 (190.9 bits), Expect = 3.6e-53, P = 3.6e-53
 Identities = 87/107 (81%), Positives = 91/107 (85%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
 Sbjct: 17 DIQMTQSPSSLSASLGERVSLTCRASQDIHGYNLFQQKPGETIKHLIYETSNLD SGVPK 76

Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSRSGSDYSL I SLES DF YYCLQYASSP TFGGGKLEIK

Sbjct: 77 RFGSRSGSDYSLIIGSLESEDFADYYCLQYASSPPTFGGGTKLEIK 123

>pir|PH1062|PH1062 Ig light chain V region (clone 202.105) - mouse (fragment)
Length = 98

Score = 415 (189.1 bits), Expect = 1.7e-52, P = 1.7e-52
Identities = 84/98 (85%), Positives = 89/98 (90%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIY+TS+L SGVPK
Sbjct: 1 DIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYSTSTLNSGVK 60
Query: 61 RFGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTF 98
RFGSRSGSDYSLTISSLES DF YYCLQYASSPYTF
Sbjct: 61 RFGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTF 98

>gp|S69053|S69053_1 anti-p-nitrophenyl phosphonate esterolytic antibody kappa
chain variable region [Mus sp.]
Length = 98

Score = 415 (189.1 bits), Expect = 1.7e-52, P = 1.7e-52
Identities = 84/98 (85%), Positives = 88/98 (89%)

Query: 8 PSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFGSR 67
PSSLSASLG+RVSLTCRASQ+I L LQQ+PDGTIKRLIY S+L SGVPKRFGSR
Sbjct: 1 PSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASLD SGVPKRFGSR 60
Query: 68 GSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGTKLE 105
GSDYSLTISSLES DF YYCLQYASSPYTFGGGTKLE
Sbjct: 61 GSDYSLTISSLESEDFADYYCLQYASSPYTFGGGTKLE 98

>pir|PL0261|PL0261 Ig kappa chain V region (anti-DNA, DP15VK) - mouse
(fragment)
Length = 88

Score = 399 (181.8 bits), Expect = 2.9e-50, P = 2.9e-50
Identities = 80/88 (90%), Positives = 83/88 (94%)

Query: 19 VSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFGSRSGSDYSLTISSL 78
VSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFGSRSGSDYSLTISSL
Sbjct: 1 VSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKRFGSRSGSDYSLTISSL 60
Query: 79 ESGDFVAYYCLQYASSPYTFGGGTKLEI 106
ES DFV YYCLQYASSP+TFGGGTKLEI
Sbjct: 61 ESEDFVDYYCLQYASSPWTFGGGTKLEI 88

>gp|U30236|MMU30236_1.Ig kappa chain [Mus musculus]
Length = 98

Score = 396 (180.4 bits), Expect = 6.7e-50, P = 6.7e-50
Identities = 81/93 (87%), Positives = 86/93 (92%)

Query: 4 MTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFS 63
MTQ+PSSLSASLG+RVSLTCRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFS
Sbjct: 4 MTQTPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLD SGVPKRFS 63
Query: 64 GSRSGSDYSLTISSLESGDFVAYYCLQYASSPY 96
GSRSGSDYSLT SSLES DFV Y CLQYASSP+
Sbjct: 64 GSRSGSDYSLTISSLESEDFVDYCLQYASSPW 96

>gp|U19320|MMU19320_1 immunoglobulin kappa light chain variable region [Mus
musculus]
Length = 97

Score = 396 (180.4 bits), Expect = 6.8e-50, P = 6.8e-50
Identities = 81/97 (83%), Positives = 85/97 (87%)

Query: 9 SSSLASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSG 68
SSLSASLG+RVSLTCRASQ+I L LQ+PDGTIKRLIYA S+L SGVPKRFSGSRSG
Sbjct: 1 SSSLASLGERVSLTCRASQEISGYLSWLQKPDGTIKRLIYAASLTDSGVPKRFSGSRSG 60

Query: 69 SDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLE 105
SDYSLTISSLES DF YYCLQYAS PYTFG GTKLE
Sbjct: 61 SDYSLTISSLESEDFADYYCLQYASPYTFGGGKLE 97

>pir|C28840|C28840 Ig kappa chain V region (HP22) - mouse (fragment)
Length = 101

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/101 (78%), Positives = 86/101 (85%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA LG+R LTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSAXLGERXXLTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
SG DYSLTISSLES DF Y CLQYASSPYTFGGGK EIK
Sbjct: 61 SGLDYSLTISSLESEDFADYXCLQYASSPYTFGGGKXEIK 101

>pir|B28840|B28840 Ig kappa chain V region (HP27) - mouse (fragment)
Length = 101

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/100 (79%), Positives = 87/100 (87%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA+LG+R SLTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSATLGERDSLTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
SG DYSLTISSLES DF YYCLQYASSPYTFGGGK I
Sbjct: 61 SGLDYSLTISSLESEDFADYYCLQYASSPYTFGGGKXXI 100

>gp|X03382|MMIGKA1_1 Mouse mRNA for GAT (HP27) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer. [Mus musculus]
Length = 100

Score = 387 (176.3 bits), Expect = 1.1e-48, P = 1.1e-48
Identities = 79/100 (79%), Positives = 87/100 (87%)

Query: 7 SPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSR 66
S SSSLSA+LG+R SLTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSR
Sbjct: 1 SLSSLSATLGERDSLTCRASQDISVYLNWLQRKLDGTIKRLIYSTSTLDSGVPKRFSGSR 60

Query: 67 SGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEI 106
SG DYSLTISSLES DF YYCLQYASSPYTFGGGK I
Sbjct: 61 SGLDYSLTISSLESEDFADYYCLQYASSPYTFGGGKXXI 100

>gp|X03383|MMIGKA2_1 Mouse mRNA for GAT (HP22) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer. [Mus musculus]
Length = 99

Score = 386 (175.9 bits), Expect = 1.6e-48, P = 1.6e-48
Identities = 78/99 (78%), Positives = 85/99 (85%)

Query: 9 SSSLASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSG 68
SSLSA LG+R /LTCRASQDI + L+ LQ++ DGTIKRLIY+TS+L SGVPKRFSGSRSG

Sbjct: 1 SSLSAXLGERXXLTCRASQDISVYLNWLQQRKLDGTIKRLIYSTSTLDSGVPKRFGSGSRSG 60

Query: 69 SDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 DYSLTISSLES DF Y CLQYASSPYTFGGGK EIK

Sbjct: 61 LDYSLTISSLESEDFADYXCLQYASSPYTFGGGTXEIK 99

>pir|D32513|D32513 Ig kappa chain precursor V region (BXW16) - mouse
 >gp|M20832|MUSIGKCLN_1 Mouse IgMk rearranged kappa light-chain mRNA
 variable region (V-J-kappa) anti-DNA autoantibody. [Mus musculus]
 Length = 129

Score = 385 (175.4 bits), Expect = 1.6e-48, P = 1.6e-48
 Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQM QSPSS+ SLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
 Sbjct: 23 DIQMIQSPSSMFGSLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 82

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSG SGSDYSLTISSLES DF YYCLQ + PYTFGGGKLEIK
 Sbjct: 83 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPYTFGGGKLEIK 129

>gp|U20061|MMU20061_1 immunoglobulin kappa chain [Mus musculus]
 Length = 108

Score = 381 (173.6 bits), Expect = 7.0e-48, P = 7.0e-48
 Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQM QSPSS+ ASLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
 Sbjct: 1 DIQMIQSPSSMFASLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSG SGSDYSLTISSLES DF YYCLQ + P TFGGGKLEIK
 Sbjct: 61 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPLTFGGGKLEIK 107

>gp|M33559|MUSIGKABE_1 Mouse Ig rearranged kappa-chain mRNA V-J2-region,
 hybridoma A6.1, partial cds. [Mus musculus]
 Length = 107

Score = 381 (173.6 bits), Expect = 7.0e-48, P = 7.0e-48
 Identities = 80/107 (74%), Positives = 86/107 (80%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQM QSPSS+ ASLG RVSL+CRASQ I NL QQ+P GTIK LIY+TS+L SGVP
 Sbjct: 1 DIQMIQSPSSMFASLGDRVSLSCRASQGIRGNLDWYQQKPGGTIKLLIYSTSNLNSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSG SGSDYSLTISSLES DF YYCLQ + P TFGGGKLEIK
 Sbjct: 61 RFGSGSGSDYSLTISSLESEDFADYYCLQRNAYPLTFGGGKLEIK 107

>pir|PL0220|PL0220 Ig kappa chain V region (G) - mouse (fragment)
 >pir|B49026|B49026 Ab2 kappa chain V region, mAb G=monoclonal
 auto-anti-idiotypic - mouse
 Length = 107

Score = 371 (169.0 bits), Expect = 1.7e-46, P = 1.7e-46
 Identities = 75/107 (70%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQ+ SSLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
 Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISVYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFGSG SG+DYSLTIS+LE D YYC QY+ P TFGGGKLEIK

11D10 Light Chain PEPTIDE - 12

Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDATYYCQYSKLPRTFGGGTKLEIK 107

>pir|D28840|D28840 Ig kappa chain V region (HP29) - mouse (fragment)
 >gp|X03384|MMIGKA3_1 Mouse mRNA for GAT (HP29) anti-idiotypic Ab2
 Ig (k) light chain against public idiotopes GAT antigen =
 Glu(60)Ala(30)Tyr(10) co-polymer. [Mus musculus]
 Length = 92

Score = 371 (169.0 bits), Expect = 1.9e-46, P = 1.9e-46
 Identities = 73/92 (79%), Positives = 82/92 (89%)

Query: 16 GQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSRSGSDYSLTI 75
 G+R SLTCRASQDI + L+ LQQ+ DGTIKRLIY+TS L SGVPKRFSRSG+DYSLTI
 Sbjct: 1 GERESLTCRASQDISVYLNWLQKLDGTIKRLIYSTSILDSGVPKRFSRSGTDYSLTI 60

Query: 76 SSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 +SLES DF Y+CLQYASSP+TFGGGKLEIK
 Sbjct: 61 NSLESEDFADYFCLQYASSPFTFGGGKLEIK 92

>gp|J00568|MUSIGKAE_1 mouse ig kappa unproductively rearranged gene: mopc173b
 v-j region. [Mus musculus]
 Length = 127

Score = 369 (168.1 bits), Expect = 2.6e-46, P = 2.6e-46
 Identities = 78/101 (77%), Positives = 82/101 (81%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
 Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIGYLNLFQQKPGETIKHLIYETSNLDSGVPK 82

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGG 101
 RFSGSRSGSDYSL I SLES DF YYCLQYASSP GG
 Sbjct: 83 RFSGSRSGSDYSLTIISLESEDFADYCLQYASSPPESEGG 123

>gp|S76654|S76654_1 F30C7 light chain variable region [Mus sp.]
 Length = 107

Score = 368 (167.7 bits), Expect = 4.3e-46, P = 4.3e-46
 Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQS SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
 Sbjct: 1 DIQMTQSSSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: # 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFSGS SG+DYSLTIS+LE D YYC QY++ P TFG GTKLE+K
 Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDATYYCQYSNLPLTFGAGTKLELK 107

>gp|M36261|MUSIGLAFP_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
 Length = 107

Score = 367 (167.2 bits), Expect = 5.8e-46, P = 5.8e-46
 Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
 DIQMTQ+ SLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
 Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESGDFVAYYCLQYASSPYTFGGGKLEIK 107
 RFSGS SG+DYSLTIS+LE D YYC QY+ P+TFGGGKLEIK
 Sbjct: 61 RFSGSGSGTDYSLTISNLEPEDATYYCQYSKLPWTFGGGKLEIK 107

>gp|X55042|MMIGKL221_1 immunoglobulin kappa light chain [Mus musculus]
 >gp|M63609|MUSIGKAVB_1 immunoglobulin kappa chain [Mus musculus]

Length = 107

Score = 300 (136.7 bits), Expect = 6.6e-46, Sum P(2) = 6.6e-46
Identities = 61/90 (67%), Positives = 71/90 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQ 90
RFGSGS SG+DYSLTIS+LE D Y+C Q
Sbjct: 61 RFGSGSGTDYSLTISNLEQEDIATYFCQQ 90

Score = 71 (32.3 bits), Expect = 6.6e-46, Sum P(2) = 6.6e-46
Identities = 14/24 (58%), Positives = 18/24 (75%)

Query: 84 VAYYCLQYASSPYTFGGGKLEIK 107
+A Y Q ++ +TFGGGKLEIK
Sbjct: 83 IATYFCQQGNTLWTFGGGKLEIK 106

>sp|P01641|KV5H_MOUSE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
>pir|A01924|KVMS3B Ig kappa chain precursor V region (VKM173B) -
mouse >gp|K00880|MUSIGKVE_1 mouse ig kappa germline v gene:
mopc173b. [Mus musculus]
Length = 117

Score = 365 (166.3 bits), Expect = 1.0e-45, P = 1.0e-45
Identities = 76/95 (80%), Positives = 80/95 (84%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSASLG+RVSLTCRASQDI L+ QQ+P TIK LIY TS+L SGVPK
Sbjct: 23 DIQMTQSPSSLSASLGERVSLTCRASQDIHGYNLNFQQKPGETIKHLIYETSNDLSGVK 82

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSP 95
RFGSGRSGSDYSL I SLES DF YYCLQYASSP
Sbjct: 83 RFGSGRSGSDYSLIIGSLESEDFADYYCLQYASSP 117

>pir|JL0080|JL0080 Ig light chain precursor V region (anti-phenyloxazolone,
18C10) - mouse (fragment) >gp|M27793|MUSIGKCPW_1 Mouse Ig active
kappa-chain mRNA V-J5 region, clone 18C10. [Mus musculus]
Length = 115

Score = 365 (166.3 bits), Expect = 1.0e-45, P = 1.0e-45
Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 7 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 66

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SG+DYSLTIS+LE D Y+C Q + PYTFGGGKLEIK
Sbjct: 67 RFGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEIK 113

>pir|A38740|A38740 Ig kappa chain V region (Py20) - mouse
Length = 111

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 73/107 (68%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
D+QMTQ+ SLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
Sbjct: 4 DVQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 63

Query: 61 RFGSGRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFGSGS SG+DYSLTIS+LE D YYC QY+ P+TFGGGKLEIK
Sbjct: 64 RFGSGSGTDYSLTISNLEPEDVATYYCQYKVPWTFGGGKLEIK 110

>sp|P01643|KV5J_MOUSE IG KAPPA CHAIN V-V REGION (MOPC 173). >pir|A01926|KVMS73
Ig kappa chain V region (MOPC 173) - mouse
Length = 108

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 73/107 (68%), Positives = 83/107 (77%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSSLASLG RV+++C ASQ IG L QQ+PDGT+K LIY TSSL SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQSIGNYLWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS L+ + YYC QY+ P TFGGGKLEIK
Sbjct: 61 RFSGSGSGTDYSLTISBLZPZBIATYYCQYQKLPRTFGGGKLEIK 107

>gp|X55044|MMIGKL229_1 immunoglobulin kappa light chain [Mus musculus]
>gp|X55045|MMIGKL233_1 immunoglobulin kappa light chain [Mus musculus]
>gp|X55046|MMIGKL38_1 immunoglobulin kappa light chain [Mus musculus]
>gp|M63611|MUSIGKAVD_1 immunoglobulin kappa chain [Mus musculus]
>gp|M63612|MUSIGKAVE_1 immunoglobulin kappa chain [Mus musculus]
>gp|M63613|MUSIGKAVF_1 immunoglobulin kappa chain [Mus musculus]
Length = 108

Score = 365 (166.3 bits), Expect = 1.1e-45, P = 1.1e-45
Identities = 74/107 (69%), Positives = 85/107 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSSLASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SG+DYSLTIS+LE D Y+C Q + PYTFGGGKLEIK
Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGKLEIK 107

>gp|U21066|MMU21066_1 immunoglobulin kappa chain variable and joining regions
[Mus musculus]
Length = 90

Score = 365 (166.3 bits), Expect = 1.3e-45, P = 1.3e-45
Identities = 73/88 (82%), Positives = 77/88 (87%)

Query: 16 GQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTI 75
G++ CRASQDIG +L+ LQQEPDGTIKRLIYATSSL SGVPKRFSGSRSGSDYSLTI
Sbjct: 3 GRKSQSHCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDGVPKRFSGSRSGSDYSLTI 62

Query: 76 SSLESQDFVAYYCLQYASSPYTFGGGK 103
SSLES DFV YYCLQYA SPYTFG GTK
Sbjct: 63 SSLESEDFVDYYCLQYAFSPYTFGSGTK 90

>gp|U16180|MMU16180_1 Ig light chain [Mus musculus]
Length = 107

Score = 364 (165.8 bits), Expect = 1.5e-45, P = 1.5e-45
Identities = 77/107 (71%), Positives = 84/107 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQM QSPSS+ A LG RVS +CRASQ NL QQ+P GTIK LIY+TS+L SGVP
Sbjct: 1 DIQMIQSPSSMFAFLGDRVSPSCRASQGKRGNDWYQQKPGGTIKLLIYSTSNLKSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLEIK 107
RFSGS SSGSDYSLTIS+LES DF YYCLQ + PYTFGGGKLEIK
Sbjct: 61 RFSGSGSGSDYSLTISTLESEDFADYYCLQRNAFYPTFGGGKLEIK 107

>gp|Z37332|HSIGVKC45_1 immunoglobulin kappa light chain variable region [Homo sapiens]
Length = 117

Score = 300 (136.7 bits), Expect = 1.6e-45, Sum P(2) = 1.6e-45
Identities = 64/101 (63%), Positives = 74/101 (73%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQSPSSLSAS+G RV++TCRASQ I L+ QQ+P K LIYA SSL SGVP
Sbjct: 1 DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGG 101
RFSGS SG+D++LTISSL+ DF YYC Q S+P GG
Sbjct: 61 RFSGSGSGTDFLTISLQPEDFATYYCQSYSTPPLTFGG 101

Score = 68 (31.0 bits), Expect = 1.6e-45, Sum P(2) = 1.6e-45
Identities = 12/17 (70%), Positives = 15/17 (88%)

Query: 91 YASSPYTFGGGKLEIK 107
Y++ P TFGGK+EIK
Sbjct: 92 YSTPPLTFGGGKVEIK 108

>gp|M36236|MUSIGLAEQ_1 immunoglobulin kappa-chain VK-1 [Mus musculus]
Length = 105

Score = 363 (165.4 bits), Expect = 2.1e-45, P = 2.1e-45
Identities = 73/105 (69%), Positives = 83/105 (79%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSLSASLG RV+++C ASQ I L+ QQ+PDGT+K LIY TSSL SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQYASSPYTFGGGKLE 105
RFSGS SG+DYSLTIS+LE D YYC QY+ PYTFGGGKLE
Sbjct: 61 RFSGSGSGTDYSLTISNLEPDIATYYCQYQSKLPYTFGGGKLE 105

>gp|X55047|MMIGKL4A1_1 immunoglobulin kappa light chain [Mus musculus]
>gp|M63674|MUSIGKAVG_1 immunoglobulin kappa chain [Mus musculus]
>gp|M63616|MUSIGKAVI_1 immunoglobulin kappa chain [Mus musculus]
Length = 107

Score = 300 (136.7 bits), Expect = 2.3e-45, Sum P(2) = 2.3e-45
Identities = 61/90 (67%), Positives = 71/90 (78%)

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60
DIQMTQ+ SSLSASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP
Sbjct: 1 DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSLESQDFVAYYCLQ 90
RFSGS SG+DYSLTIS+LE D Y+C Q
Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQ 90

Score = 67 (30.5 bits), Expect = 2.3e-45, Sum P(2) = 2.3e-45
Identities = 14/24 (58%), Positives = 17/24 (70%)

Query: 84 VAYYCLQYASSPYTFGGGKLEIK 107
+A Y Q ++ TFGGKLEIK
Sbjct: 83 IATYFCQQGNTLRTFGGKLEIK 106

>pir|S38862|S38862 Ig kappa chain V region - mouse >gp|X75854|MMIGKC1_1
immunoglobulin variable kappa light chain [Mus musculus]
Length = 108

Score = 299 (136.2 bits), Expect = 4.3e-45, Sum P(2) = 4.3e-45
Identities = 62/101 (61%), Positives = 75/101 (74%)

11D10 Light Chain PEPTIDE – 16

Query: 1 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEPDGTIKRLIYATSSLGSGVPK 60

D+QMTQ+ SSL+ASLG RV+++CRASQDI L+ QQ+PDGT+K LIY TS L SGVP

Sbjct: 1 DVQMTQTSSLAASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Query: 61 RFSGSRSGSDYSLTISSESGDFVAYYCLQYASSPYTFGGG 101

RFSGS SG+DYSLTIS+LE D Y+C Q + P GG

Sbjct: 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPPWTFGG 101

S. Chatterjee

```
===== 2006
Return-Path: <blastmai@BLASTER.NLM.NIH.GOV>
Received: from UKCC (NJE origin SMTP@UKCC) by UKCC.UKY.EDU (LMail V1.2a/1.8a) with BSMTTP id 2242; Fri,
19 Jan 1996 17:16:15 -0500
Received: from ncbi.nlm.nih.gov by UKCC.uky.edu (IBM VM SMTP V2R3) with TCP;
Fri, 19 Jan 96 17:16:12 EST
Received: from blaster.nlm.nih.gov by ncbi.nlm.nih.gov
id RAA27387; Fri, 19 Jan 1996 17:15:58 -0500
Received: by blaster.nlm.nih.gov (950511.SGI.8.6.12.PATCH526/5.6)
id RAA04498; Fri, 19 Jan 1996 17:15:57 -0500
Date: Fri, 19 Jan 1996 17:15:57 -0500
Message-Id: <199601192215.RAA04498@blaster.nlm.nih.gov>
To: SKCHAT00@UKCC.uky.edu
Subject: Results-BLAST Server
From: NCBI BLAST E-Mail Server <blast@ncbi.nlm.nih.gov>
Errors-To: <owner-blast@ncbi.nlm.nih.gov>
Reply-To: "NCBI BLAST E-Mail Server" <blast@ncbi.nlm.nih.gov>
```

```
=-+=====
To Obtain Documentation: send an e-mail message to 'blast@ncbi.nlm.nih.gov'
with the word HELP in the body of the message. The documentation was last
modified March 18th.
```

```
=-+=====
March 18, 1995
The BLAST FAQ was updated with the question Q33 related to degenerated
nucleotide code available for the BLAST programs.
```

```
=-+=====
August 8, 1995
A new server directive ACKNOWLEDGE, has been added to the server. See the
help file for more details.
```

```
Trying blaster... connected
National Center for Biotechnology Information (NCBI)
```

Experimental GENINFO(R) BLAST Network Service (Blaster)

Fri Jan 19 17:14:36 EST 1996, Up 30 days, 5:05, 1 user, load: 22.91, 24.88, 20.67

PEPTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+SwissProt+PIR+SPUpdate+GenPept+GUPdate, updated daily
for efficient, complete searches of the five component databases:
pdb      Brookhaven Protein Data Bank, April 1995 Release
swissprot SWISS-PROT Release 32.0, December 1995
pir       PIR Release 45.0 (complete), June 30, 1995
spupdate  SWISS-PROT cumulative weekly update to the major release
genpept   CDS translations from GenBank(R) Release 92, December 15, 1995
gpupdate  cumulative daily updates to the major release of genpept
kabatpro  Kabat Sequences of Proteins of Immunological Interest, June 1995
tfd       TFD transcription factor (protein) database Release 7.0, June 1993
alu *     Translations of select Alu repeats from REPBASE
```

NUCLEOTIDE SEQUENCE DATABASES

```
nr Non-redundant PDB+GBUpdate+GenBank+EmblUpdate+EMBL, updated daily
for efficient, complete searches of the four component databases:
pdb      Brookhaven Protein Data Bank, April 1995 Release
genbank   GenBank(R) Release 92 (no daily updates), December 15, 1995
gbupdate  GenBank(R) cumulative daily updates to the major release
embl      EMBL Data Library, Release 45.0, December 1995
emblu     EMBL Data Library cumulative daily updates to the major release
vector    Vector subset of GenBank(R), February 3rd, 1995
alu **    Select Alu repeats from REPBASE
kabatnuc  Kabat Sequences of Nucleic Acid of Immunological Interest, June 1995
epd       Eukaryotic Promoter Database Release 43, June 1995
dbest +   Database of Expressed Sequence Tags (cumulative daily update)
dbsts +   Database of Sequence Tagged Sites Release 1.5, October 26, 1994
```

- * Databases that are not accessible through the NCBI Retrieve E-mail server.
+ The TBLASTX program is restricted to searching these databases.

You can obtain the BLAST documentation files, send a message consisting of just the word "help" (without the quotes) to: blast@ncbi.nlm.nih.gov
Last modification dates: August 10th 95 for the E-mail server help, January 19th 94 for the BLAST manual and March 18th 95 for the BLAST FAQ.

For a free subscription to "NCBI News", the NCBI newsletter, send a request along with your name and postal mailing address to: info@ncbi.nlm.nih.gov

A new GenBank sequence submission tool, called BankIt, is now available through the NCBI's home page on the World Wide Web. The URL is <http://www.ncbi.nlm.nih.gov/>

BLASTN 1.4.8MP [20-June-1995] [Build 08:41:09 Oct 19 1995]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. *J. Mol. Biol.* 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= 11D10VL.nuc
(321 letters)

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL
662,343 sequences; 449,479,361 total letters.

```
Searching.....done
```

Observed Numbers of Database Sequences Satisfying Various EXPECTation Thresholds (E parameter values)

Histogram units: = 4 Sequences : less than 4 sequences

EXPECTation Threshold
(E parameter)

Observed Counts-->

10000	4088	197	=====
6310	3891	178	=====
3980	3713	78	=====
2510	3635	99	=====
1580	3536	51	=====
1000	3485	41	=====
631	3444	22	=====
398	3422	21	=====
251	3401	16	=====
158	3385	63	=====
100	3322	19	=====
63.1	3303	14	=====
39.8	3289	22	=====
25.1	3267	16	=====
15.8	3251	5	=====

```
>>>>>>>>>>>>>>>> Expect = 10.0, Observed = 3246 <<<<<<<<<<<<<<<<
10.0 3246 6 |=
6.31 3240 13 ==
3.98 3227 11 ==
2.51 3216 4 =
1.58 3212 12 ===
1.00 3200 20 =====
0.63 3180 6 =
0.40 3174 5 =
0.25 3169 9 ==
0.16 3160 5 =
```

0.10	3155	10	==
0.063	3145	4	=
0.040	3141	5	=
0.025	3136	8	==
0.016	3128	7	=
0.010	3121	6	=
0.0063	3115	7	=
0.0040	3108	3	:
0.0025	3105	2	:
0.0016	3103	2	:

Sequences producing High-scoring Segment Pairs:			High Score	Smallest Sum Probability P(N)	N
gb L41880	MUSIKCC	Mus musculus immunoglobulin kappa c...	1533	2.4e-122	1
gb L48667	MUSX	Mus musculus (cell line C3H/F2-15) ...	1517	6.3e-121	1
gb J00565	MUSIGKAC1	Mouse ig kappa active gene: vk41 v-...	1488	7.7e-119	1
emb V00808	MMIGK7	Part of the murine gene for kappa-i...	1479	4.3e-118	1
gb I03643	I03643	Sequence 4 from patent US 4642334. ...	1479	9.1e-118	1
gb M59920	MUSIGKAA3	Mouse IG germline chain mRNA V-J re...	1464	1.6e-116	1
gb M36246	MUSIGLAFA	Mouse Ig kappa-chain mRNA V region,...	1445	6.6e-115	1
emb Z22118	MDIGKVBS	M.domesticus IgK variable region.	1434	5.1e-114	1
gb M64168	MUSIGKAF	Mouse Ig active kappa-chain mRNA V-...	1407	9.4e-112	1
emb X02177	MMIGGVJ1	M.musculus mRNA for IgG kappa light...	1362	4.2e-108	1
gb U29617	MMU29617	Mus musculus anti-DNA antibody Ig k...	1357	1.5e-107	1
gb J00566	MUSIGKVC	Mouse ig kappa germline v gene: vk4...	1351	2.0e-107	1
gb U25098	MMU25098	Mus musculus anti-Pseudomonas aerug...	1353	2.7e-107	1
emb X02178	MMIGGVJ2	M.musculus mRNA for IgG kappa light...	1335	7.4e-106	1
emb X63811	MMVKMRB11	M.musculus mRNA for IgM V(k)MRB11	1332	1.8e-105	1
gb M12191	MUSIGKCA	Mouse Ig active kappa-chain VJ2C mR...	1326	4.1e-105	1
gb S69053	S69053	Ig V kappa =anti-p-nitrophenyl phos...	1326	5.3e-105	1
gb U30236	MMU19326	Mus musculus anti-DNA antibody Ig k...	1297	1.4e-102	1
gb S55170	S55170	nitrophenyl phosphonate-specific an...	1290	4.8e-102	1
emb X03382	MMIGKGA1	Mouse mRNA for GAT (HP27) anti-idio...	1289	6.2e-102	1
gb J00568	MUSIGKAE	mouse ig kappa unproductively rearr...	1177	7.2e-101	2
gb U19320	MMU19320	Mus musculus immunoglobulin kappa l...	1276	7.7e-101	1
emb X03383	MMIGKGA2	Mouse mRNA for GAT (HP22) anti-idio...	1270	2.4e-100	1
gb U21066	MMU21066	Mus musculus immunoglobulin kappa c...	1121	1.3e-98	2
gb L22571	MUSIGKAF2	Mouse IgK chain mRNA V-region.	557	1.5e-97	5
gb M20832	MUSIGKCLN	Mouse IgMk rearranged kappa light-c...	1200	1.2e-94	1
gb U20061	MMU20061	Mus musculus anti-DNA antibody immu...	1191	8.2e-94	1
gb M33559	MUSIGKABE	Mouse Ig rearranged kappa-chain mRN...	1191	8.3e-94	1
gb K00880	MUSIGKVE	mouse ig kappa germline v gene: mop...	1180	1.3e-91	1
gb U16180	MMU16180	Mus musculus anti-cardiolipin antib...	1137	2.6e-89	1
emb X03384	MMIGKGA3	Mouse mRNA for GAT (HP29) anti-idio...	1137	3.0e-89	1
gb U19327	MMU19327	Mus musculus immunoglobulin kappa l...	1129	1.5e-88	1
gb U19326	MMU19326	Mus musculus immunoglobulin kappa l...	1086	5.9e-85	1
gb M36236	MUSIGLAER	Mouse Ig kappa-chain mRNA V region,...	1027	3.7e-80	1
gb M84436	MUSIGLBM	Mouse rearranged light chain variab...	1011	7.0e-79	1
gb M27793	MUSIGKCPW	Mouse Ig active kappa-chain mRNA V-...	1011	7.3e-79	1
gb M63611	MUSIGKAVD	Mouse Ig rearranged kappa-chain (V-...	1011	7.7e-79	1
gb M63609	MUSIGKAVB	Mouse Ig rearranged kappa-chain (V-...	832	2.6e-78	2
gb U20820	MMU20820	Mus musculus Ig Fab F9.13.7 light c...	993	2.4e-77	1
gb M36261	MUSIGLAFF	Mouse Ig kappa-chain mRNA V region,...	993	2.5e-77	1
gb M63614	MUSIGKAVG	Mouse Ig rearranged kappa-chain (V-...	832	8.0e-77	2
emb X70090	MMNL4H10	M.musculus NL4H10 mRNA for immunogl...	986	9.4e-77	1
gb M60020	MUSIGKAAAM	Mouse Ig kappa chain mRNA V-J regio...	984	1.1e-76	1
gb S50261	S50261	Ig VL=anti-CD4 mAb M-T151 variable ...	984	1.2e-76	1
gb M84440	MUSIGLCC	Mouse rearranged light chain variab...	984	1.2e-76	1
emb X65095	MMIGLC151	M.musculus mRNA for IG light chain ...	984	1.4e-76	1
gb S76654	S76654	Ig VL=F30C7 light chain variable re...	984	1.4e-76	1
gb M36242	MUSIGLAEW	Mouse Ig kappa-chain mRNA V region,...	979	3.6e-76	1
emb X85995	HSDELIGVJ	H.sapiens mRNA for immunoglobulin k...	975	6.4e-76	1
gb M84434	MUSIGLAC	Mouse rearranged light chain variab...	975	6.9e-76	1
gb S74560	S74560	Ig V kappa =rheumatoid factor RF3-2...	973	1.1e-75	1
gb K00745	MUSIGKAAO	Mouse Ig kappa active V-region: ant...	965	5.2e-75	1

gb	L35316	MUSIVJR	Mus musculus germline immunoglobuli...	957	2.0e-74	1
gb	M84442	MUSIGLCH	Mouse rearranged light chain variab...	957	2.2e-74	1
gb	M63608	MUSIGKAVA	Mouse Ig rearranged kappa-chain (V-...	957	2.4e-74	1
gb	S77025	S77025	Ig VL=H2A/H2B-specific antibody lig...	952	6.3e-74	1
gb	S63022	S63022	anti-ganglioside GD3 immunoglobulin...	948	1.1e-73	1
gb	M60019	MUSIGKAAAL	Mouse Ig kappa chain mRNA V-J regio...	948	1.1e-73	1
gb	M31911	MUSIGKCRM	Mouse Ig light-chain V-J region mRN...	948	1.3e-73	1
emb	X68119	MMIGHPS4B	M.musculus gene for IgK light chain...	948	1.3e-73	1
emb	X06111	MMIGKVJ2	Mouse (hVH65-107) mRNA for immunogl...	948	1.3e-73	1
gb	M32043	MUSIGKCRT	Mouse Ig kappa-chain mRNA V-J regio...	941	5.1e-73	1
emb	X64163	HSFOG1L	H.sapiens mRNA for Fog1L kappa ligh...	939	6.3e-73	1
gb	U16689	MMU16689	Mus musculus Ig light chain leader ...	939	6.4e-73	1
gb	M17160	MUSIGKCKO	Mouse Ig kappa-chain mRNA V-region ...	939	6.7e-73	1
gb	U07211	MMU07211	Mus musculus clone 101 anti-C5a Ig ...	939	7.5e-73	1
gb	M63610	MUSIGKAVC	Mouse Ig rearranged kappa-chain (V-...	939	7.5e-73	1
gb	M20278	MUSIGKCOA	Mouse Ig active kappa chain mRNA V-...	939	7.5e-73	1
emb	X68113	MMIGHPS1B	M.musculus gene for IgK light chain...	939	7.5e-73	1
gb	M34590	MUSIGKABT	Mouse Ig kappa-chain mRNA V-J regio...	939	7.6e-73	1
emb	X05796	MMIGVK36	Mouse hybridoma 36-65 Ig L-chain re...	939	7.6e-73	1
gb	M37020	MUSIGKADS	Mouse Ig rearranged kappa-chain mRN...	939	7.6e-73	1
gb	M37021	MUSIGKADT	Mouse Ig rearranged kappa-chain mRN...	939	7.6e-73	1
emb	X53329	MMHS2H1VL	M.musculus/ H.sapiens chimeric anti...	938	2.5e-72	1
gb	M92336	MUSIGKVJE	Mouse immunoglobulin kappa light-ch...	932	2.7e-72	1
gb	M92332	MUSIGKVJC	Mouse immunoglobulin kappa light-ch...	932	2.8e-72	1
gb	M32040	MUSIGKCRQ	Mouse Ig kappa-chain mRNA V-J regio...	932	2.9e-72	1
gb	U27000	MMU27000	Mus musculus, isolate 3-7 Vk, Ig va...	930	2.9e-72	1
gb	U05217	MMU05217	Mus musculus Balb/c anti-platelet i...	930	3.6e-72	1
emb	X72463	HSIGKLV42	H.sapiens mRNA for rearranged Ig ka...	930	3.6e-72	1
gb	M85256	HUMIGKVJ	Human IgK anti-platelet integrin II...	930	4.2e-72	1
gb	S77030	S77030	Ig V kappa =H4-specific antibody li...	930	4.2e-72	1
emb	X68115	MMIGHPS2B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68121	MMIGHPS5B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68123	MMIGHPS6B	M.musculus gene for IgK light chain...	930	4.2e-72	1
emb	X68125	MMIGHPS7B	M.musculus gene for IgK light chain...	930	4.2e-72	1
gb	M31258	MUSIGKCRZ	Mouse active rheumatoid factor IgK ...	930	4.3e-72	1
gb	U24115	MMU24115	Mus musculus immunoglobulin F9.13.7...	927	5.2e-72	1
emb	X75854	MMIGKC1	M.musculus IgG1 mRNA for immunoglob...	787	6.0e-72	2
emb	X57639	MMMAVLC	M.musculus mRNA for monoclonal anti...	927	7.7e-72	1
gb	S60859	S60859	Ab2 kappa chain V region mAb 24 (...)	927	8.1e-72	1
gb	L39092	MUSIGK527A	Mus musculus (clone 5-27) anti-fluo...	925	9.4e-72	1
gb	M31915	MUSIGKCRO	Mouse Ig light-chain V-J region mRN...	923	1.6e-71	1
gb	M29534	SYNIGHAD	Mouse heavy-chain and lambda-chain ...	921	1.6e-71	1
gb	U30238	MMU30238	Mus musculus anti-DNA antibody Ig k...	922	2.0e-71	1
dbj	D29934	MUSLCATS14	Mouse mRNA for light chain of anti-...	921	2.3e-71	1
gb	M31906	MUSIGKCRJ	Mouse Ig light-chain V-J region mRN...	921	2.4e-71	1
gb	M31910	MUSIGKCRJ	Mouse Ig light-chain V-J region mRN...	921	2.4e-71	1
gb	I11959	I11959	Sequence 71 from patent US 5416202.	921	2.4e-71	1
gb	I11962	I11962	Sequence 74 from patent US 5416202.	921	2.4e-71	1

WARNING: Descriptions of 3146 database sequences were not reported due to the limiting value of parameter V = 100.

>gb|L41880|MUSIKCC Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.
Length = 390

Plus Strand HSPs:

Score = 1533 (423.6 bits), Expect = 2.4e-122, P = 2.4e-122
Identities = 313/321 (97%), Positives = 313/321 (97%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
|||||
Sbjct: 67 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126

Query: 61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
|||||

Sbjct: 127 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 186
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||||
 Sbjct: 187 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAA 246
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||||
 Sbjct: 247 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
 |||||||
 Sbjct: 307 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 366
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||||
 Sbjct: 367 GGGACCAAGCTGGAAATAAAA 387

>gb|L48667|MUSX Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA
 antibody light chain mRNA.
 Length = 324

Plus Strand HSPs:

Score = 1517 (419.2 bits), Expect = 6.3e-121, P = 6.3e-121
 Identities = 311/321 (96%), Positives = 311/321 (96%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||||
 Sbjct: 1 GANATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
 Query: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 120
 |||||||
 Sbjct: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||||
 Sbjct: 121 GATGGAACTTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAA 180
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
 |||||||
 Sbjct: 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTGTCCGTACACGTTTCGGAGGG 300
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||||
 Sbjct: 301 GGGACCAAGCTGGAAATAAAA 321

>gb|J00565|MUSIGKAC1 Mouse ig kappa active gene: vk41 v-j region.
 Length = 684

Plus Strand HSPs:

Score = 1488 (411.2 bits), Expect = 7.7e-119, P = 7.7e-119
 Identities = 308/321 (95%), Positives = 308/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||||
 Sbjct: 313 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 372
 Query: 61 CTCACCTTGTGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 120
 |||||||
 Sbjct: 373 CTCACCTTGTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 432

Query: 121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180
 |||
 Sbjct: 433 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAA 492
 |||
 Query: 181 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 493 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 552
 |||
 Query: 241 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||
 Sbjct: 553 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 612
 |||
 Query: 301 GGCACCAAGCTGGAAATAAA 321
 |||
 Sbjct: 613 GGCACCAAGCTGGAAATCAA 633

>emb|V00808|MMIGK7 Part of the murine gene for kappa-immunoglobulin leader
 peptide and variable part (cell line MOPC41).
 Length = 685

Plus Strand HSPs:

Score = 1479 (408.7 bits), Expect = 4.3e-118, P = 4.3e-118
 Identities = 307/321 (95%), Positives = 307/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373
 |||
 Query: 61 CTCAC TTGTGCGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 374 CTCAC TTGTGCGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 433
 |||
 Query: 121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180
 |||
 Sbjct: 434 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAA 493
 |||
 Query: 181 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 494 AGGTTCA GTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553
 |||
 Query: 241 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||
 Sbjct: 554 GAAGATTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 613
 |||
 Query: 301 GGCACCAAGCTGGAAATAAA 321
 |||
 Sbjct: 614 GGCACCAAGCTGGAAATCAA 634

>gb|103643|103643 Sequence 4 from patent US 4642334. >gb|107835|107835 Sequence
 4 from patent EP 0088994.
 Length = 324

Plus Strand HSPs:

Score = 1479 (408.7 bits), Expect = 9.1e-118, P = 9.1e-118
 Identities = 307/321 (95%), Positives = 307/321 (95%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
 |||
 Query: 61 CTCAC TTGTGCGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 61 CTCAC TTGTGCGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
 |||
 Query: 121 GATGGAAC TATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAA 180

```

Sbjct: 121 |||||GATGGA|ACTATTA|AAACGC|CTGATCTACGCC|ACATCCAGTTAGATTCTGGTGTCCCAAA 180
Query: 181 AGGTT|CAGTGG|CAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Sbjct: 181 |||||AGGTT|CAGTGG|CAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGG 300
Sbjct: 241 |||||GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGA 300
Query: 301 GGGACCAAGCTGGAATAAAA 321
Sbjct: 301 |||||GGACCAAGCTGGAATCAAA 321

```

>gb|M59920|MUSIGKAA3 Mouse Ig germline chain mRNA V-J region, partial cds.
Length = 321

Plus Strand HSPs:

Score = 1464 (404.5 bits), Expect = 1.6e-116, P = 1.6e-116
Identities = 304/318 (95%), Positives = 304/318 (95%), Strand = Plus / Plus

```

Query: 4 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTC 63
Sbjct: 1 ATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTC 60
Query: 64 ACTTGT|CGGGCAAGTCAGGACATTGGTATTA|AACTTACATTGGCTTCAGCAGGAACCAGAT 123
Sbjct: 61 ACTTGT|CGGGCAAGTCAGGACATTGGTAGT|AGCTTAACTGGCTTCAGCAGGAACCAGAC 120
Query: 124 GGA|ACTATTA|AAACGCCTGATCTACGCC|ACATCCAGTTTAGGTTCTGGTGTCCCAAAAGG 183
Sbjct: 121 GGA|ACTATTA|AAACGCCTGATCTACGCC|ACATCCAGTTTAGATTCTGGTGTCCCAAAAGG 180
Query: 184 TTCAGTGGCAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 243
Sbjct: 181 TTCAGTGGCAGTAGGTCTGGGT|CAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAA 240
Query: 244 GATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGGGGG 303
Sbjct: 241 GATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACGTTCCGGTGGAGGC 300
Query: 304 ACCAAGCTGGAATAAAA 321
Sbjct: 301 ACCAAGCTGGAATCAAA 318

```

>gb|M36246|MUSIGLAFA Mouse Ig kappa-chain mRNA V region, partial cds, from
hybridoma H220-23.
Length = 303

Plus Strand HSPs:

Score = 1445 (399.3 bits), Expect = 6.6e-115, P = 6.6e-115
Identities = 295/303 (97%), Positives = 295/303 (97%), Strand = Plus / Plus

```

Query: 19 TCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGGGCAAGT 78
Sbjct: 1 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGT 60
Query: 79 CAGGACATTGGTATTA|AACTTACATTGGCTTCAGCAGGAACCAGATGGA|ACTATTAACGC 138
Sbjct: 61 CAGGACATTGGTAGT|AGCTTAACTGGCTTCAGCAGGAACCAGATGGA|ACTATTAACGC 120
Query: 139 CTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTT|CAGTGGCAGTAGG 198
Sbjct: 121 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAAAGGTT|CAGTGGCAGTAGG 180

```

```

Query: 199 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGCCTAT 258
      |||
Sbjct: 181 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGACTAT 240

Query: 259 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATA 318
      |||
Sbjct: 241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGNAATA 300

Query: 319 AAA 321
      |||
Sbjct: 301 AAA 303

```

>emb|222118|MDIGKVS M.domesticus IgK variable region.
Length = 321

Plus Strand HSPs:

Score = 1434 (396.2 bits), Expect = 5.1e-114, P = 5.1e-114
Identities = 302/321 (94%), Positives = 302/321 (94%), Strand = Plus / Plus

```

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
      |||
Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60

Query: 61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
      |||
Sbjct: 61 CTCACCTGTGCGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
      |||
Sbjct: 121 GATGGAACATTAAACGCCTGATCTACAGCACATCCACTTTAAATTCTGGTGTCCCAAAA 180

Query: 181 AGGTTTCAGTGGCAGTAGGTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
      |||
Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
      |||
Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300

Query: 301 GGGACCAAGCTGGAATAAAA 321
      |||
Sbjct: 301 GGGACCAAACTGGAATAAAA 321

```

>gb|M64168|MUSIGKFT Mouse Ig active kappa-chain mRNA V-region.
Length = 306

Plus Strand HSPs:

Score = 1407 (388.8 bits), Expect = 9.4e-112, P = 9.4e-112
Identities = 291/303 (96%), Positives = 291/303 (96%), Strand = Plus / Plus

```

Query: 19 TCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGCGGCAAGT 78
      |||
Sbjct: 4 TCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGCGGCAAGT 63

Query: 79 CAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 138
      |||
Sbjct: 64 CAGGACATTGGTAATAGCTAAACTGGCTTCAGCAGGAACCAGATGGAACATTAAACGC 123

Query: 139 CTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGG 198
      |||
Sbjct: 124 CTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAAAGGTTTCAGTGGCAGTAGG 183

Query: 199 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTGTAGCCTAT 258
      |||

```

Sbjct: 184 TCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAATCTGAAGATTTTGTAGTCTAT 243
 Query: 259 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACCAAGCTGGAATA 318
 |||||
 Sbjct: 244 TACTGTCTACAATATGCTAGTTATACGTACACGTTCCGAGGGGGGACCAAGTTGGAATA 303
 Query: 319 AAA 321
 |||
 Sbjct: 304 AAA 306

>emb|X02177|MMIGGVJ1 M.musculus mRNA for IgG kappa light chain (partial) Gloop
 1
 Length = 380

Plus Strand HSPs:

Score = 1362 (376.3 bits), Expect = 4.2e-108, P = 4.2e-108
 Identities = 294/321 (91%), Positives = 294/321 (91%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 42 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 101
 Query: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 102 CTCACCTGTGCGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 161
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 162 GATGGAACATTAAACGCCTGATCTACGCCCATCCACTTTAGATTCTGGTGTCCCAAAA 221
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 222 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 281
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 282 GAAGATTTTCAGACTATTACTGTCTACAATATCTTAGTTATCCGCTCACGTTCCGGTGCT 341
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 342 GGGACCAAGCTGGAGCTGAAA 362

>gb|U29617|MMU29617 Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J
 region, hybridoma 52-46A, partial cds.
 Length = 285

Plus Strand HSPs:

Score = 1357 (375.0 bits), Expect = 1.5e-107, P = 1.5e-107
 Identities = 277/284 (97%), Positives = 277/284 (97%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
 Query: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 CTCACCTGTGCGGCAAGTCAGGACATTGGTAGCTTAACTGGCTTCAGCAGGAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 121 GATGGAACATTAAACGCCTGATCTACGCCCATCCAGTTTAGATTCTGGTGTCCCAAAA 180
 Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC 284
 |||
 Sbjct: 241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCC 284

>gb|J00566|MUSIGKVC Mouse ig kappa germline v gene: vk41. >emb|V00804|MMIGK3
 Murine kappa-immunoglobulin gene fragment including signal peptide
 and variable region.
 Length = 664

Plus Strand HSPs:

Score = 1351 (373.3 bits), Expect = 2.0e-107, P = 2.0e-107
 Identities = 279/290 (96%), Positives = 279/290 (96%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 314 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 373

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 374 CTCACCTGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCA 433

Query: 121 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||
 Sbjct: 434 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAA 493

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 494 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 553

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAC 290
 |||
 Sbjct: 554 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCTCCAC 603

>gb|U25098|MMU25098 Mus musculus anti-Pseudomonas aeruginosa serotype IATS O6
 lipopolysaccharide O-antigen, Ig light chain variable region mRNA,
 partial cds.
 Length = 336

Plus Strand HSPs:

Score = 1353 (373.9 bits), Expect = 2.7e-107, P = 2.7e-107
 Identities = 293/321 (91%), Positives = 293/321 (91%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||
 Sbjct: 1 GAGCTCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||
 Sbjct: 61 CTCACCTGTCTGGGCAAGTCAGGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCA 120

Query: 121 GATGGAACATTTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||
 Sbjct: 121 GATGGAACATTTAAACGCCTGATCTACGCCGATCCACTTTAGATTCTGGTGTCCCAAA 180

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||
 Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTATCCGCTGACGTTCCGGTGCT 300

Query: 301 GGGACCAAGCTGGAATAAAA 321
 |||

Sbjct: 301 GGGACCAAGCTGGAGCTGAAA 321

>emb|X02178|MMIGGVJ2 M.musculus mRNA for IgG kappa light chain (partial) Gloop
2
Length = 381

Plus Strand HSPs:

Score = 1335 (368.9 bits), Expect = 7.4e-106, P = 7.4e-106
Identities = 291/321 (90%), Positives = 291/321 (90%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          |||
Sbjct:  43 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 102
          |||

Query:   61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          |||
Sbjct: 103 CTCACCTGTGCGGGCAAGTCAAGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGGAACCA 162
          |||

Query:   121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAAA 180
          |||
Sbjct: 163 GATGGAACATTAAACGCCTGATCTACGCCCATCCACTTAGATTCTGGTGTCCCAAAA 222
          |||

Query:   181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          |||
Sbjct: 223 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 282
          |||

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          |||
Sbjct: 283 GAAGATTTTGCAGACTATTATTGTCTACAATATCTAGTTATCCGCTCACGTTCCGGTGCT 342
          |||

Query:   301 GGGACCAAGCTGGAAATAAAA 321
          |||
Sbjct:  343 GGGACCAAGCTGGAGCTGAAA 363
          |||

```

>emb|X63811|MMVKMRB11 M.musculus mRNA for IgM V(k)MRB11
Length = 279

Plus Strand HSPs:

Score = 1332 (368.1 bits), Expect = 1.8e-105, P = 1.8e-105
Identities = 272/279 (97%), Positives = 272/279 (97%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          |||
Sbjct:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 60
          |||

Query:   61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          |||
Sbjct:   61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA 120
          |||

Query:   121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCAAAA 180
          |||
Sbjct:  121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTAGATTCTGGTGTCCCAAAA 180
          |||

Query:   181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          |||
Sbjct:  181 AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          |||

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGT 279
          |||
Sbjct:  241 GAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGT 279
          |||

```

>gb|M12191|MUSIGKMA Mouse Ig active kappa-chain VJ2C mRNA from plasmacytoma
MOPC 173B, partial cds.
Length = 383

Plus Strand HSPs:

Score = 1326 (366.4 bits), Expect = 4.1e-105, P = 4.1e-105
 Identities = 290/321 (90%), Positives = 290/321 (90%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          |||
Sbjct:  51 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 110

Query:   61 CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          |||
Sbjct: 111 CTCACATGCCGGGCAAGTCAGGACATTGATGGTTATTTAACTTGTTCAGCAGAAACCA 170

Query:   121 GATGGAAGTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
          |||
Sbjct: 171 GGTGAAAGTATTAACACCTGATCTATGAAACATCCAATTTAGATTCTGGTGTCCCAAAA 230

Query:   181 AGGTTCAAGTGGCAGTAGGTTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          |||
Sbjct: 231 AGGTTCAAGTGGCAGTAGGTTGGGTCAGATTATTCTCTCATTATCGGCAGCCTTGAGTCT 290

Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGG 300
          |||
Sbjct: 291 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCCTCCACGTTGCGAGGG 350

Query:   301 GGGACCAAGCTGGAAATAAAA 321
          |||
Sbjct: 351 GGGACCAAGCTGGAAATAAAA 371

```

>gb|S69053|S69053 Ig V kappa =anti-p-nitrophenyl phosphonate esterolytic
 antibody kappa chain variable region (clone CNJ206) [mice, mRNA
 Partial, 295 nt].
 Length = 295

Plus Strand HSPs:

Score = 1326 (366.4 bits), Expect = 5.3e-105, P = 5.3e-105
 Identities = 278/294 (94%), Positives = 278/294 (94%), Strand = Plus / Plus

```

Query:   21 TCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTGGGCAAGTCA 80
          |||
Sbjct:   1 TCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTGGGCAAGTCA 60

Query:   81 GGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAAGTATTAACGCCT 140
          |||
Sbjct:   61 GGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAAGTATTAACGCCT 120

Query:   141 GATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAAAGGTTCAAGTGGCAGTAGGTC 200
          |||
Sbjct:  121 GATCTACGCCGCATCCACTTTAGATTCTGGTGTCCCAAAAAGGTTCAAGTGGCAGTAGGTC 180

Query:   201 TGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTA 260
          |||
Sbjct:  181 TGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGCAGACTATTA 240

Query:   261 CTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGGGGACCAAGCTGGA 314
          |||
Sbjct:  241 CTGTCTACAATATGCTAGTTCTCCGTACACGTTGCGAGGGGGACCAAGCTGGA 294

```

>gb|U30236|MMU30236 Mus musculus anti-DNA antibody Ig kappa chain mRNA, V-J
 region, hybridoma 84.32, partial cds.
 Length = 293

Plus Strand HSPs:

Score = 1297 (358.4 bits), Expect = 1.4e-102, P = 1.4e-102

Identities = 269/281 (95%), Positives = 269/281 (95%), Strand = Plus / Plus

```

Query:   6 CCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCAC 65
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   6 CCTGATGACCCAGACTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCAC 65

Query:  66 TTGTCGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCAGATGG 125
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  66 TTGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCAGATGG 125

Query: 126 AACTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCTCCAAAGGTT 185
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 126 AACTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCTCCAAAGGTT 185

Query: 186 CAGTGGCAGTAGGCTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGA 245
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 186 CAGTGGCAGTAGGCTCTGGGTGAGATTATTCTCTCACCAGCAGCCTTGAGTCTGAAGA 245

Query: 246 TTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGT 286
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 246 TTTTGTAGACTATTCTGTCTACAATATGCTAGTTCTCCGT 286

```

>gb|S55170|S55170 nitrophenyl phosphonate-specific antibody 48G7 light chain VJ
[mice, Genomic, 324 nt].
Length = 324

Plus Strand HSPs:

Score = 1290 (356.5 bits), Expect = 4.8e-102, P = 4.8e-102
Identities = 286/321 (89%), Positives = 286/321 (89%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   4 GAGCTCGTGCTACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 63

Query:  61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  64 CTCACCTGTCTGGGCAAGTCAGGAAATTAATGGTTACTTAGGCTGGCTTCAGCAGAAACCA 123

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCTCCAAA 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 124 GATGGAACATTAAACGCCTGATCTACGCCCATCCACTTACATTCTGGTGTCCTCCAAA 183

Query: 181 AGGTTTCAGTGGCAGTAGGCTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 184 AGGTTTCAGTGGCAGTAGGCTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 243

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 244 GAAGATTTTGCACTATTACTGTCTGCAATATGCTAGTTATCTCGGACGTTCCGGTGA 303

Query: 301 GGGACCAAGCTGGAATAAAA 321
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 304 GGCACCAAACTGGAATCAAAA 324

```

>emb|X03382|MMIGKA1 Mouse mRNA for GAT (HP27) anti-idiotypic Ab2 Ig (k) light
chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10)
co-polymer
Length = 303

Plus Strand HSPs:

Score = 1289 (356.2 bits), Expect = 6.2e-102, P = 6.2e-102
Identities = 277/302 (91%), Positives = 277/302 (91%), Strand = Plus / Plus

```

Query:   19 TCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGT 78
          |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Sbjct:      1 TCTCTATCTTCCTTATCTGCCACTCTGGGAGAAAGAGACAGTCTCACTTGTCTGGGCAAGT 60
Query:      79 CAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCAAGTGGAACTATTAAACGC 138
             |||||
Sbjct:      61 CAGGATATTAGTGTCTTAACTGGCTTCAGCGGAAACTAGATGGAACCTATTAAACGC 120
Query:     139 CTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAGGTTCAAGTGGCAGTAGG 198
             |||||
Sbjct:     121 CTGATCTACAGCACATCCACTTTAGATTCTGGTGTCCCAAAAGGTTCAAGTGGCAGTAGG 180
Query:     199 TCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTAT 258
             |||||
Sbjct:     181 TCTGGGTTAGATTATCTCTCACCATCAGCAGCCTAGAGTCTGAAGATTTTGCAGACTAT 240
Query:     259 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGGGGGACCAAGCTGGAAATA 318
             |||||
Sbjct:     241 TACTGTCTACAATATGCTAGTTCTCCGTACACGTTCTGGAGGGGGGACCAAGCNGGNAATA 300
Query:     319 AA 320
             ||
Sbjct:     301 AA 302

```

>gb|J00568|MUSIGKAE mouse ig kappa unproductively rearranged gene: mopc173b v-j region. >emb|V00760|MMIG04 Mouse pseudogene for kappa-immunoglobulin.
Length = 1157

Plus Strand KSPs:

Score = 1177 (325.2 bits), Expect = 7.2e-101, Sum P(2) = 7.2e-101
Identities = 257/284 (90%), Positives = 257/284 (90%), Strand = Plus / Plus

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||
Sbjct:     547 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT  606
             |||

Query:     61  CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACATTACATTGGCTTCAGCAGGAACCA  120
             |||
Sbjct:    607  CTCACCTGCCGGGCAAGTCAGGACATTCATGGTATTTAACTTGTTTCAGCAGAAACCA  666
             |||

Query:    121  GATGGAACATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA  180
             |||
Sbjct:    667  GGTGAAACATTAACACCTGATCTATGAAACATCCAATTTAGATTCTGGTGTCCCAAAA  726
             |||

Query:    181  AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||
Sbjct:    727  AGGTTCAAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCATTATCGGCAGCCTTGAGTCT  786
             |||

Query:    241  GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC  284
             |||
Sbjct:    787  GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAGTTCTCC  830
             |||

```

Score = 170 (47.0 bits), Expect = 7.2e-101, Sum P(2) = 7.2e-101
Identities = 34/34 (100%), Positives = 34/34 (100%), Strand = Plus / Plus

Query: 288 CACGTTTCGGAGGGGGGACCAAGCTGGAATAAAA 321
 |||
 Sbjct: 833 CACGTTTCGGAGGGGGGACCAAGCTGGAATAAAA 866

>gb|U19320|MMU19320 Mus musculus immunoglobulin kappa light chain variable
region mRNA, clone MRL2-117, partial cds.
Length = 293

Plus Strand HSPs:

Score = 1276 (352.6 bits), Expect = 7.7e-101, P = 7.7e-101
Identities = 272/293 (92%), Positives = 272/293 (92%), Strand = Plus / Plus

```

Query:   25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGAC 84
          |||
Sbjct:   1  TCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGAA 60

Query:   85 ATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGCCTGATC 144
          |||
Sbjct:   61 ATTAGTGGTTACTTAAGCTGGCTTCAGCAAAAACCAGATGGAACATTAAACGCCTGATC 120

Query:   145 TACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 204
          |||
Sbjct:   121 TACGCCGCATCCACTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 180

Query:   205 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGT 264
          |||
Sbjct:   181 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGT 240

Query:   265 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAAT 317
          |||
Sbjct:   241 CTACAATATGCTAGTTATCCGTATACGTTTCGGATCGGGGACCAAGCTGGAAAT 293

```

>emb|X03383|MMIGKA2 Mouse mRNA for GAT (HP22) anti-idiotypic Ab2 Ig (k) light chain against public idiotopes GAT antigen = Glu(60)Ala(30)Tyr(10) co-polymer
Length = 297

Plus Strand HSPs:

Score = 1270 (350.9 bits), Expect = 2.4e-100, P = 2.4e-100
Identities = 272/297 (91%), Positives = 272/297 (91%), Strand = Plus / Plus

```

Query:   25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGAC 84
          |||
Sbjct:   1  TCTTCCTTATCTGCCNCTCTGGGAGAAAGAGNCNGTCTCACTTGTCTGGGCAAGTCAGGAT 60

Query:   85 ATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGAACATTAAACGCCTGATC 144
          |||
Sbjct:   61 ATTAGTGGTTACTTAAACTGGCTTCAGCGGAAACTAGATGGAACATTAAACGCCTGATC 120

Query:   145 TACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 204
          |||
Sbjct:   121 TACAGCACATCCACTTTAGATTCTGGTGTCCCCAAAAGGTTTCAGTGGCAGTAGGTCTGGG 180

Query:   205 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGT 264
          |||
Sbjct:   181 TTAGATTATTCTCTCACCATCAGCAGCCTAGAGTCTGAAGATTTTGCAGACTATTNCTGT 240

Query:   265 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAAATAAAA 321
          |||
Sbjct:   241 CTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCNGGAAATAAAA 297

```

>gb|U21066|MMU21066 Mus musculus immunoglobulin kappa chain V-J regions mRNA, clone MRL3-7, partial cds.
Length = 273

Plus Strand HSPs:

Score = 1121 (309.8 bits), Expect = 1.3e-98, Sum P(2) = 1.3e-98
Identities = 233/244 (95%), Positives = 233/244 (95%), Strand = Plus / Plus

```

Query:   67 TGTCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGA 126
          |||
Sbjct:   30 TGTCGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCAGATGGA 89

Query:   127 ACTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTTC 186
          |||
Sbjct:   90 ACTATTAACGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCCAAAAGGTTTC 149

```

Query: 187 AGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 246
 |||
 Sbjct: 150 AGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 209

Query: 247 TTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGGGGGACC 306
 |||
 Sbjct: 210 TTTGTAGACTATTACTGTCTACAATATGCTTTTCTCCGTATACGTTCCGATCGGGGACC 269

Query: 307 AAGC 310
 |||
 Sbjct: 270 AAGC 273

Score = 141 (39.0 bits), Expect = 1.3e-98, Sum P(2) = 1.3e-98
 Identities = 29/30 (96%), Positives = 29/30 (96%), Strand = Plus / Plus

Query: 37 GCCTCTCTGGGACAAAGAGTCAGTCTCACT 66
 |||
 Sbjct: 1 GCCTCTCTGGGAGAAAGAGTCAGTCTCACT 30

>gb|L22571|MUSIGKAF2 Mouse IgK chain mRNA V-region.
 Length = 270

Plus Strand HSPs:

Score = 557 (153.9 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 117/124 (94%), Positives = 117/124 (94%), Strand = Plus / Plus

Query: 177 CAAAAGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGA 236
 |||
 Sbjct: 147 CCAAAGGTTCAAGTGGCAGTAGGTCTGGGTCAGATCATTTCTCACCATCACCAGCCTTGA 206

Query: 237 GTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCG 296
 |||
 Sbjct: 207 GTCTGAAGATTTTGTAGACTATTACTGTCTTCAATATGTTAGTTCTCCGTACACGTTCCG 266

Query: 297 AGGG 300
 |||
 Sbjct: 267 AGGG 270

Score = 398 (110.0 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 86/94 (91%), Positives = 86/94 (91%), Strand = Plus / Plus

Query: 25 TCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGAC 84
 |||
 Sbjct: 1 TCCTCCTTATCTGCCTCTCTGGGAGAGAGAGTCAGTCTCACTTGTCTGGGCAAGTCAGGAC 60

Query: 85 ATTGGTATTAACCTTACATTGGCTTCAAGAGGAC 118
 |||
 Sbjct: 61 ATTGGTAATAGCTTAACTGGCTTCAACAGGAGC 94

Score = 111 (30.7 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 23/24 (95%), Positives = 23/24 (95%), Strand = Plus / Plus

Query: 132 TAAACGCCTGATCTACGCCACATC 155
 |||
 Sbjct: 106 TTAACGCCTGATCTACGCCACATC 129

Score = 91 (25.1 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 19/20 (95%), Positives = 19/20 (95%), Strand = Plus / Plus

Query: 156 CAGTTTAGGTTCTGGGTGTC 175
 |||
 Sbjct: 129 CAGTTTAGATTCTGGGTGTC 148

Score = 82 (22.7 bits), Expect = 1.5e-97, Sum P(5) = 1.5e-97
 Identities = 18/20 (90%), Positives = 18/20 (90%), Strand = Plus / Plus

Query: 115 GAACCAGATGGAACATTAA 134
 |||||
 Sbjct: 90 GGAGCAGATGGAACATTAA 109

>gb|M20832|MUSIGKLN Mouse IgMk rearranged kappa light-chain mRNA variable
 region (V-J-kappa) anti-DNA autoantibody.
 Length = 413

Plus Strand HSPs:

Score = 1200 (331.6 bits), Expect = 1.2e-94, P = 1.2e-94
 Identities = 276/321 (85%), Positives = 276/321 (85%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 93 GACATCCAGATGATTAGTCAGTCTCCATCGTCCATGTTTGGCTCTCTGGGAGACAGAGTCAGT 152
 Query: 61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 153 CTCTCTTGTCCGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 212
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 213 GGTGGAACATTAAACTCCTGATCTACTCCACATCCAATTTAAATCTGGTGTCCCATCA 272
 Query: 181 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 273 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTAGAGTCT 332
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 333 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCGTATCCGTACACGTTCCGAGGG 392
 Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 393 GGGACCAAGCTGGAAATAAAA 413

>gb|U20061|MMU20061 Mus musculus anti-DNA antibody immunoglobulin kappa chain
 mRNA, clone A6.1Vkappa, partial cds.
 Length = 324

Plus Strand HSPs:

Score = 1191 (329.1 bits), Expect = 8.2e-94, P = 8.2e-94
 Identities = 275/321 (85%), Positives = 275/321 (85%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GACATCCAGATGATTAGTCAGTCTCCATCGTCCATGTTTGCCTCTCTGGGAGACAGAGTCAGT 60
 Query: 61 CTCACCTTGTCTGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 CTCTCTTGTCTGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCA 120
 Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA 180
 |||||
 Sbjct: 121 GGTGGAACATTAAACTCCTGATCTACTCCACATCCAATTTAAATCTGGTGTCCCATCA 180
 Query: 181 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTTCAGTGGCAGTAGGTCCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTAGAGTCT 240
 Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 241 GAAGATTTTGCAGACTATTACTGTCTACAGCGTAATGCGTATCCCTCTCACGTTCCGAGGG 300
 Query: 301 GGGACCAAGCTGGAAATAAAA 321

11D10 Light Chain NUCLEOTIDE - 20

Score = 1129 (312.0 bits), Expect = 1.5e-88, P = 1.5e-88
Identities = 241/260 (92%), Positives = 241/260 (92%), Strand = Plus / Plus

```
Query:   55 GTCAGTCTCACTTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAG 114
          |||
Sbjct:   1  GTCAGTCTCACTTGTCTGGGCAAGTCAGGACATTGGTAAATAGCTTAACTGGCTTCAGCAG 60

Query:  115 GAACCAGATGGAACATTAACACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTC 174
          |||
Sbjct:  61 GAACCAGATGGAACATTAACACGCCTGATCTATGCCACATCCAGATTAGATTTTGATGTC 120

Query:  175 CCCAAAAGGTTTCAGTGGCAGTAGGTCTGGGTCTCAGATTATTCTCTCACCATCAGCAGCCTT 234
          |||
Sbjct:  121 CCCAAAAGGTTTCAGTGGCAGTAGGTCTGGGTCTCAGATTATTCTCTCACCATCAGCAGCCTT 180

Query:  235 GAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTT 294
          |||
Sbjct:  181 GAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGGTAGTTTTCGGCTCACGTTT 240

Query:  295 GGAGGGGGGACCAAGCTGGA 314
          |||
Sbjct:  241 GGTGCTGGGACCAAGCTGGA 260
```

>gb|U19326|MMU19326 Mus musculus immunoglobulin kappa light chain variable region mRNA, clone MRL2-169, partial cds.
Length = 246

Plus Strand HSPs:

Score = 1086 (300.1 bits), Expect = 5.9e-85, P = 5.9e-85
Identities = 230/246 (93%), Positives = 230/246 (93%), Strand = Plus / Plus

```
Query:   67 TGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCAGATGGA 126
          |||
Sbjct:   1  TGTCTGGGCAAGTCAGGACATTGGTAGTAGCTTAACTGGCTTCAGCAGGAACCAGATGGA 60

Query:  127 ACTATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCTCCAAAAGGTTT 186
          |||
Sbjct:  61 ACTATTAACGCCTGATCTACGCCACATCCAGATTAGATTCTGGTGTCCTCCGAAAGGTTT 120

Query:  187 AGTGGCAGTAGGTCTGGGTCTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 246
          |||
Sbjct:  121 AGTGGCAGTAGGTCTGGGTCTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGAT 180

Query:  247 TTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTGGAGGGGGGACC 306
          |||
Sbjct:  181 TTTGTAGACTATTACTGTCAACAATATGGTAGTTTTCGGCTCACGTTTGGGTCTGGGACC 240

Query:  307 AAGCTG 312
          |||
Sbjct:  241 AAGCTG 246
```

>gb|M36236|MUSIGLAEQ Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma H130-5VK.
Length = 317

Plus Strand HSPs:

Score = 1027 (283.8 bits), Expect = 3.7e-80, P = 3.7e-80
Identities = 255/317 (80%), Positives = 255/317 (80%), Strand = Plus / Plus

```
Query:   1  GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          |||
Sbjct:   1  GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGATCACC 60

Query:  61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
          |||
```

```
Sbjct:      61 ATCAGTTGCACTGCAAGTCAGGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA 120
Query:     121 GATGGAAC TATTAAACGCCTGATCTACGCCACATCCAGTTT AGGTTCTGGTGCCCCAAA 180
          ||| ||||| ||||| ||||| ||||| ||||| ||| ||| |||||
Sbjct:     121 GATGGAAC TGTTAAACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 180
Query:     181 AGGTTTCAGTGGCAGTAGGCTCGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||| ||| |||||
Sbjct:     181 AGGTTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGAACCCTGGAACCT 240
Query:     241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTT CGGAGGG 300
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:     241 GAAGATA TTGCCACTTACTATTGTCAGCAGTATAGTAAGCTT CCGTACACGTT CGGAGGG 300
Query:     301 GGGACCAAGCTGGAAAT 317
          ||| ||||| ||||| |||||
Sbjct:     301 GGGACCAAGCTGGAAAT 317
```

>gb|M84436|MUSIGLBM Mouse rearranged light chain variable region gene sequence.
Length = 360

Plus Strand HSPs:

Score = 1011 (279.4 bits), Expect = 7.0e-79, P = 7.0e-79
Identities = 255/321 (79%), Positives = 255/321 (79%), Strand = Plus / Plus

```

Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT   60
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     10 GATGTCCAGATGACACAGTCTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC   69

Query:     61 CTCAC TTGTCGGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA   120
             ||| ||| | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     70 ATCAGTTGCAGTGCAAGTCAGGGCATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA   129

Query:    121 GATGGAAC TATTA AACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA   180
             ||| | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    130 GATGGAAC TGTTAA ACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA   189

Query:    181 AGGTT CAGTGGCAGTAGGTCTGGGT CAGATTAT TCTCTCACCATCAGCAGCCTTGAGTCT   240
             ||| | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    190 AGGTT CAGTGGCAGTGGGTCTGGGACAGATTAT TCTCTCACCATCAGCAACCTGGAACCT   249

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG   300
             ||| | | | | | | | | | | | | | | | | | | | |
Sbjct:    250 GAAGAT GTTGCCACTTATTATTGT CAGCAATATAGTAAGGTTCCGTGGACGTT CGGTGGA   309

Query:    301 GGGACCAAGCTGGAAATAAAA   321
Sbjct:    310 GGCACCAAGCTGGAAATCAA   330

```

>gb|M27793|MUSIGKCPW Mouse Ig active kappa-chain mRNA V-J5 region, clone 18C10.
Length = 345

Plus Strand HSPs:

Score = 1011 (279.4 bits), Expect = 7.3e-79, P = 7.3e-79
Identities = 255/321 (79%), Positives = 255/321 (79%), Strand = Plus / Plus

[illegible]

Sbjct: 139 GATGGAAGCTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 198
Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
Sbjct: 199 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 258
Query: 241 GAAGATTTTGAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG 300
Sbjct: 259 GAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCTGACACGTTTCGGAGGG 318
Query: 301 GGGACCAAGCTGGAAATAAAA 321
Sbjct: 319 GGGACCAAGCTGGAAATAAAA 339

```
>gb|M63611|MUSIGKAVD Mouse Ig rearranged kappa-chain (V-I dCR J2) gene V10-J
region, hybridoma KL2.29, partial cds. >gb|M63612|MUSIGKAVE Mouse
Ig rearranged kappa-chain (V-I dCR J2) gene V10-J region, hybridoma
KL2.33, partial cds. >gb|M63613|MUSIGKAVF Mouse Ig rearranged
kappa-chain (V-I dCR J2) gene V10-J region, hybridoma KL3.8, partial
cds. >emb|X55044|MMIGKL229 M.musculus gene for immunoglobulin kappa
light chain variable region (KL2.29) >emb|X55045|MMIGKL233
M.musculus gene for immunoglobulin kappa light chain variable
region (KL2.33) >emb|X55046|MMIGKL38 M.musculus gene for
immunoglobulin kappa light chain variable region (KL3.8)
Length = 324
```

Plus Strand HSPs:

Score = 1011 (279.4 bits), Expect = 7.7e-79, P = 7.7e-79
Identities = 255/321 (79%), Positives = 255/321 (79%), Strand = Plus / Plus

[illegible]

>gb|M63609|MUSIGKAVB Mouse Ig rearranged kappa-chain (V-I dCR J1) gene V10-J region, hybridoma KL2.21, partial cds. >emb|X55042|MMIGKL221 M.musculus gene for immunoglobulin kappa light chain variable region (KL2.21)
Length = 321

Plus Strand HSPs:

Score = 832 (229.9 bits), Expect = 2.6e-78, Sum P(2) = 2.6e-78
Identities = 212/269 (78%), Positives = 212/269 (78%), Strand = Plus / Plus

```
Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT   60  
            ||| | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct:     1 GATATCCAGATGACACAGACTACATCCTCCTGTCTGCCTCTCTGGGAGACAGAGTCACC   60  
  
Query:    61 CTCAC TTGTCGGGCAAGTCAGGACATTGGTATTAAC TTACATTGGCTTCAGCAGGAACCA   120  
           ||| | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct:    61 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAAACTGGTATCAGCAGAAAACA   120  
  
Query:   121 GATGGAAC TATTA AACGCCCTGATCTACGCCACATCCAGTTTTAGGTTCTGGTGCCCCAAA   180  
           ||| | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct:   121 GATGGAAC GTTAA ACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA   180  
  
Query:   181 AGG TTCAGTGGCAGTAGGTCTGGGTCAGATTAT TCTCTCACCATCAGCAGCCTTGAGTCT   240  
           ||| | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct:   181 AGG TTCAGTGGCAGTGGGTC TGGAACAGATTAT TCTCTCACCAT TAGCAACTGGAGCAA   240  
  
Query:   241 GAAGATTTTGTAGCCTATTACTGTCTACA   269  
           ||| | | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct:   241 GAAGATATTGCCACTTACTTTT GCCAACA   269
```

Score = 184 (50.8 bits), Expect = 2.6e-78, Sum P(2) = 2.6e-78
Identities = 56/80 (70%), Positives = 56/80 (70%), Strand = Plus / Plus

Query: 242 AAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGGAGGGG 301
Sbjct: 239 AAGAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTGTGGACGTTCCGGTGGAG 298

Query: 302 GGACCAAGCTGGAAATAAAA 321
Sbjct: 299 GCACCAAGCTGGAAATCAAA 318

```
>gb|U20820|MMU20820 Mus musculus Ig Fab F9.13.7 light chain mRNA, partial cds.
      Length = 330
```

Plus Strand HSPs:

Score = 993 (274.4 bits), Expect = 2.4e-77, P = 2.4e-77
Identities = 253/321 (78%), Positives = 253/321 (78%), Strand = Plus / Plus

[illegible]

```
>gb|M36261|MUSIGLAPP Mouse Ig kappa-chain mRNA V region, partial cds, from
    hybridoma L2-10C1.
    Length = 321
```

Score = 993 (274.4 bits), Expect = 2.5e-77, P = 2.5e-77
Identities = 253/321 (78%), Positives = 253/321 (78%), Strand = Plus / Plus

```
Query:      1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT   60
             ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     1 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC   60

Query:    61 CTCAC TTGT CGGGA AGT CAGG ACATT GGT ATTA ACT TACA TTGG CTTC AGCA GGA ACCA   120
           ||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    61 ATCAG TTG CAG TGCA AGT CAGG GCATT AGCA ATTATT TAA ACTGGT ATCAG CAGA AACCA   120

Query:    121 GATGGA ACTAT TAAC GCCTG ATCTAC GCCACA TCCAGTTTAG GTTCTGGTGTCCCCAAA   180
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    121 GATGGA ACTGT TAA ACTCCTG ATCTAT TACA CATCA AGTTTAC ACTCAG GAGTCCCATCA   180

Query:    181 AGGTT CAGTGG CAGTAG GTCTGGG TCAGATTAT TCTCTC ACCATC AGCAG CCTTGAGTCT   240
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    181 AGGTT CAGTGG CAGTGGG TCGGG ACAGATTAT TCTCTC ACCATC AGCAA CCTGGAACCT   240

Query:    241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG   300
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    241 GAAGATATTGCCACTTACTATTGTCTCAGCAGTATAGTAAGCTTCCGTGGACGTTCGGTGGA   300

Query:    301 GGGACCAAGCTGGAAATAAAA   321
           ||||| ||||| ||||| |||||
Sbjct:    301 GGCACCAAGCTGGAAATCAAA   321
```

>gb|M63614|MUSIGKAVG Mouse Ig rearranged kappa-chain (V-IdCR J1) gene V10-J region, hybridoma KL4A1, partial cds. >gb|M63616|MUSIGKAVI Mouse Ig rearranged kappa-chain (V-IdCR J1) gene V10-J region, hybridoma KL4C8, partial cds. >emb|X55047|MMIGKL4A1 M.musculus gene for immunoglobulin kappa light chain variable region (KL4A1)
Length = 321

Score = 832 (229.9 bits), Expect = 8.0e-77, Sum P(2) = 8.0e-77
Identities = 212/269 (78%), Positives = 212/269 (78%), Strand = Plus / Plus

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||
Sbjct:      1  GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC  60

Query:     61  CTCACTTGTGCGGCAAGTCAGGACATTGGTATTAACATTACATTGGCTTCAGCAGGAACCA  120
             |||||
Sbjct:     61  ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAACTGGTATCAGCAGAAACCA  120

Query:    121  GATGGAACATTATAAACGCCCTGATCTACGCCACATCCAGTTTATGGTTCTGGTGTCCCAAA  180
             |||||
Sbjct:    121  GATGGAACGTGTTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA  180

Query:    181  AGGTTTCAGTGGCAGTAGGTCGGGTGAGATTATCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||||
Sbjct:    181  AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATCTCTCACCATTAGCAACTGGAGCAA  240

Query:    241  GAAGATTTTGTAGCCTATTACTGTCTACA  269
             |||||
Sbjct:    241  GAAGATATTGCCACTTACTTTGCCAACA  269

```

Score = 166 (45.9 bits), Expect = 8.0e-77, Sum P(2) = 8.0e-77
Identities = 54/80 (67%), Positives = 54/80 (67%), Strand = Plus / Plus

Query: 242 AAGATTTTGTAGCCTATTACTGTCACAATATGCTAGTTCTCCGTACACGTTCGGAGGGG 301
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 239 AAGAAGATATTGCCACTTACTTTGCCAACAGGGTAATACGCTTCGGACGTTTCGGTGAAG 298

Query: 302 GGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 299 GCACCAAGCTGGAAATCAA 318

>emb|x70090|MMNL4H10 M.musculus NL4H10 mRNA for immunoglobulin light chain,
 variable region
 Length = 321

Plus Strand HSPs:

Score = 986 (272.4 bits), Expect = 9.4e-77, P = 9.4e-77
 Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 1 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 60

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 61 ATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTACACTGGTATCAGCAGAAACAA 120

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||
 Sbjct: 121 GATGGAACGTAAACTNCTGATCTACTACACTAAGATTACATTCAGGAGTCCCATCA 180

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 181 AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAA 240

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 241 GAAGATATTGCCACTTACTTTTGCCAACAGGCTAATACGCTTCGTACACGTTCCGAGGG 300

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||
 Sbjct: 301 GGGACCAAGCTGGAAATAAA 321

>gb|M60020|MUSIGKAAAM Mouse Ig kappa chain mRNA V-J region, 5' end.
 Length = 395

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.1e-76, P = 1.1e-76
 Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

Query: 1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
 |||||
 Sbjct: 72 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 131

Query: 61 CTCACCTGTCTGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA 120
 |||||
 Sbjct: 132 ATCAGTTGCAGTGCAAGTCAGGGCATTAGTAATTATTAACTGGTATCAGCAGAAACCA 191

Query: 121 GATGGAACATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
 |||||
 Sbjct: 192 GATGGAACGTAAACTCCTGATCTATTACACATCAAGATTACACTCAGGAGTCCCATCA 251

Query: 181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
 |||||
 Sbjct: 252 AGGTTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT 311

Query: 241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
 |||||
 Sbjct: 312 GAAGATATTGCCACTTATTTTGTGAGCAGTATAGTAAGTCCCATTCACGTTCCGGCTCG 371

Query: 301 GGGACCAAGCTGGAAATAAAA 321
 |||||

>gb|S50261|S50261 Ig VL=anti-CD4 mAb M-T151 variable region light chain (J2,
chimeric antibody) [mice, hybridoma cells, mRNA Partial, 381 nt].
Length = 381

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.2e-76, P = 1.2e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

[illegible]

>gb|M84440|MUSIGLCC Mouse rearranged light chain variable region gene sequence.
Length = 360

Plus Strand HSPs:

Score = 984 (271.9 bits), Expect = 1.2e-76, P = 1.2e-76
Identities = 252/321 (78%), Positives = 252/321 (78%), Strand = Plus / Plus

[illegible]

Plus Strand HSPs:

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||
Sbjct:      1  GATATCCAGATGACACAGACTATATCCTCCCTCTCTGCCTCTCTGGGAGACAGAGTCACC  60

Query:     61  CTCACCTGTGCGGCAAGTCAGGACATTGGTATTAACCTACATTGGCFTTCAGCAGGAACCA  120
             ||| ||| |||
Sbjct:     61  ATCAGTTGCAGGGCAAGTCAGGACATTAACAATTATTTAAGCTGGTATCAGCAGAAACCA  120

Query:    121  GATGGAACATATTAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA  180
             |||
Sbjct:    121  GATGGAACATGTTAAACTCCTGATCTACTACACATCAAGATTACATTAGGAGTCCCATCA  180

Query:    181  AGGTTCAAGTGGCAGTAGGTCTGGGTCAAGTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||
Sbjct:    181  AGGTTCAAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTACCAACCTGGAGCAA  240

Query:    241  GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG  300
             |||
Sbjct:    241  GAAGATGTTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTACACGTTTCGGAGGG  300

Query:    301  GGGACCAAGCTGGAATAAAA  321
             |||
Sbjct:    301  GGGACCAAGCTGGAATAAAA  321

```

Plus Strand HSPs:

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||
Sbjct:      1  GATATTAGATGACACAGTCTTCATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC  60

Query:      61  CTCACCTGTGCGGGCAAGTCAGGACATTGGTATTAACCTACATTGGCTTCAGCAGGAACCA  120
             |||||
Sbjct:      61  ATCAGTTGCAGGGCAAGTCAGGATATTAGCAATTATTTAAACTGGTATCAGCAGAAACCA  120

Query:      121  GATGGAACATTATAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA  180
             |||||
Sbjct:      121  GATGGAACGTATAAACTCCTGATCTACTACACATCAAGATTAACTCAGGAGTCCCATCA  180

Query:      181  AGGTTCAAGTGGCAGTAGGTCTGGGTGAGTATTCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||||
Sbjct:      181  AGGTTCAAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACTGGAACCT  240

Query:      241  GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG  300
             |||||
Sbjct:      241  GAAGATATTGCCACTTACTATTGTCAGCAGTATAGTAACCTTCCGCTCAGGTTTCGGTGCT  300

Query:      301  GGGACCAAGCTGGAATAAAA  321
             |||||
Sbjct:      301  GGGACCAAGCTGGAGCTGAAA  321

```

>gb|M36242|MUSIGLAEW Mouse Ig kappa-chain mRNA V region, partial cds, from

Plus Strand HSPs:

```
>emb|X85995|HSDELIGVJ H.sapiens mRNA for immunoglobulin kappa light chain
variable region (patient DEL)
Length = 388
```

Plus Strand HSPs:

>gb|M84434|MUSIGLAC Mouse rearranged light chain variable region gene sequence.
Length = 360

```

Query:      1  GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT  60
             |||||||
Sbjct:     67  GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC  126

Query:     61  CTCACCTTGTCGGGCAAGTCAGGACATTGGTATTAACATTACATTGGCTTCAGCAGGAACCA  120
             |||||||
Sbjct:    127  ATCACTTGCCAGGCGAGTCAGGACATTAGTAATTAATTTAAATTGGTATCAGCAGAAACCA  186

Query:    121  GATGGAACATTAACACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAAA  180
             |||||||
Sbjct:    187  GGGAAAGCCCTTAAGCTCCTGATCCACGCTGCATCCAGTTTGGAACACAGGGGTCCCATCA  246

Query:    181  AGGTTCAAGTGGCAGTAGGTCTGGGTCAGATTATCTCTCACCATCAGCAGCCTTGAGTCT  240
             |||||||
Sbjct:    247  AGGTTCAAGTGGGAGTGGGCTGGGACAGATTTTCTTTACCATCAGCAGCCTACAGCCT  306

Query:    241  GAAGATTTTGATGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGG  300
             |||||||
Sbjct:    307  GAAGATCTTGCAACATATTACTGCCAACAGTATGATAATCTCCGCTCACTTTCGGCGGG  366

Query:    301  GGGACCAAGCTGGAAATAAAA 321
             |||||||
Sbjct:    367  GGGACCAAGGTGGAGATCAA 387

```

11D10 Light Chain NUCLEOTIDE - 29

Plus Strand HSPs:

Score = 975 (269.4 bits), Expect = 6.9e-76, P = 6.9e-76
Identities = 251/321 (78%), Positives = 251/321 (78%), Strand = Plus / Plus

```

Query:   1 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 60
          || || ||||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  10 GATGTCATGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGAGTCACC 69

Query:   61 CTCACCTGTCGGGCAAGTCAGGACATTGGTATTAACCTTACATTGGCTTCAGCAGGAACCA 120
          ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   70 ATCAGTTGCAGTGAAGTCAGGGCATTAGCAATTATTTAACTGGTATCAGCATAAACCA 129

Query:  121 GATGGAACCTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  130 GATGGAACCTGTTAACTCCTGATCTATTACACATCAAGTTTACACTCAGGAGTCCCATCA 189

Query:  181 AGGTTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  190 AGGTTTCAGTGGCAGTGGGTCTGGGACAGATTATTCTCTCACCATCAGCAACCTGGAACCT 249

Query:  241 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCCGAGGG 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:  250 GAAGATGTTGCCACTTATTATTGTCTAGCAATATAGTAAGGTTCCGTGGACGTTCCGGTGA 309

Query:  301 GGGACCAAGCTGGAATAAAA 321
          || ||||| ||||| |||||
Sbjct:  310 GGCACCAAGCTGGAATCAAA 330

```

WARNING: HSPs involving 3196 database sequences were not reported due to the limiting value of parameter B = 50.

Parameters:

V=100
B=50
H=1
-qtype
E=10

-ctxfactor=2.00

Query	Strand	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Lambda	Computed K	----- H
+1	0	+5,-4	0.192	0.173	0.357	same	same	same	
-1	0	+5,-4	0.192	0.173	0.357	same	same	same	

Query	Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
+1	0	321	321	321	10.	116	11	N/A	73	0.022	76
-1	0	321	321	321	10.	116	11	N/A	73	0.022	76

Statistics:

Query	Strand	MatID	Expected High Score	Observed High Score	HSPs Reportable	HSPs Reported
+1	0	123 (34.0 bits)	1533 (423.6 bits)	4005	58	
-1	0	123 (34.0 bits)	741 (204.8 bits)	18	0	

Query	Strand	MatID	Neighborhd Words	Word Hits	Excluded Hits	Failed Extensions	Successful Extensions	Overlaps Excluded
+1	0	314	56657	18407	32829	5475	85	
-1	0	314	37893	3357	33503	1084	5	

Database: Non-redundant PDB+GBupdate+GenBank+EMBLupdate+EMBL

Release date: 6:31 AM EST Jan 19, 1996

Posted date: 6:39 AM EST Jan 19, 1996

of letters in database: 449,479,361

of sequences in database: 662,343

of database sequences satisfying E: 3246
No. of states in DFA: 220 (220 KB)
Total size of DFA: 228 KB (256 KB)
Time to generate neighborhood: 0.02u 0.01s 0.03t Real: 00:00:00
No. of processors used: 3
Time to search database: 27.36u 3.37s 30.73t Real: 00:00:40
Total cpu time: 27.49u 3.46s 30.95t Real: 00:00:41

WARNINGS ISSUED: 2

WEST**End of Result Set**

Generate Collection

Print

L1: Entry 1 of 1

File: USPT

Aug 14, 2001

US-PAT-NO: 6274143

DOCUMENT-IDENTIFIER: US 6274143 B1

TITLE: Methods of delaying development of HMFG-associated tumors using anti-idiotypic antibody 11D10

DATE-ISSUED: August 14, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Chatterjee; Malaya	Lexington	KY	40502	
Foon; Kenneth A.	Lexington	KY	40536	

US-CL-CURRENT: 424/155.1; 424/131.1, 424/138.1, 424/139.1, 424/143.1, 424/156.1, 424/174.1, 530/387.2

CLAIMS:

What is claimed is:

1. A method of delaying development of a human milk fat globule (HMFG)-associated tumor in an individual having a low tumor burden of an HMFG-associated tumor, comprising administering to the individual an amount of anti-idiotypic antibody 11D10 sufficient to delay development of said HMFG-associated tumor, wherein 11D10 is produced by a hybridoma cell line deposited at the American Type Culture Collection (ATCC) as Accession No. HB 12020, or progeny thereof, whereby development of said HMFG-associated tumor is delayed.
2. The method of claim 1, wherein the individual is high risk of development of an HMFG-associated tumor.
3. The method of claim 2, wherein the individual is in an adjuvant setting.
4. The method of claim 1, wherein 11D10 is administered with an adjuvant.
5. The method of claim 4, wherein the adjuvant is aluminum hydroxide.
6. The method of claim 1, wherein the HMFG-associated tumor is a breast tumor.
7. The method of claim 1, wherein 11D10 is administered in an amount of about 1 mg to about 4 mg.
8. The method of claim 1, wherein 11D10 is administered in an amount of about 2 mg.
9. The method of claim 1, wherein 11D10 is administered at weekly intervals.
10. The method of claim 1, wherein 11D10 is administered every two weeks.
11. The method of claim 1, wherein 11D10 is heat-treated prior to administration.
12. A method of treatment of a human milk fat globule (HMFG)-associated tumor in

an individual with a low tumor burden of an HMFG-associated tumor, comprising administering to the individual an amount of anti-idiotypic antibody 11D10 sufficient to treat said HMFG-associated tumor, wherein 11D10 is produced by a hybridoma cell line deposited at the American Type Culture Collection (ATCC) as Accession No. HB 12020, or progeny thereof, whereby said HMFG-associated tumor is treated.

13. The method of claim 12, wherein the individual is high risk of development of an HMFG-associated tumor.

14. The method of claim 13, wherein the individual is in an adjuvant setting.

15. The method of claim 12, wherein 11D10 is administered with an adjuvant.

16. The method of claim 15, wherein the adjuvant is aluminum hydroxide.

17. The method of claim 12, wherein the HMFG-associated tumor is a breast tumor.

18. The method of claim 12, wherein 11D10 is administered in an amount of about 1 mg to about 4 mg.

19. The method of claim 12, wherein 11D10 is administered in an amount of about 2 mg.

20. The method of claim 12, wherein 11D10 is administered at weekly intervals.

21. The method of claim 12, wherein 11D10 is administered every two weeks.

22. The method of claim 12, wherein 11D10 is heat-treated prior to administration.

23. The method of claim 1, wherein the antibody has light and heavy chain variable region amino acid sequences in SEQ ID NO:2 and SEQ ID NO:4, respectively.

24. The method of claim 12, wherein the antibody has light and heavy chain variable region amino acid sequences in SEQ ID NO:2 and SEQ ID NO:4, respectively.